

FORM PTO-1390  
(REV 10-95)

U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES  
DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1779

U.S. APPLICATION NO. (If known, see 37 CFR §1.5)

09/673400

INTERNATIONAL APPLICATION NO.

INTERNATIONAL FILING DATE

PCT/DE99/01178

15 April 1999

PRIORITY DATE CLAIMED

17 April 1998

TITLE OF INVENTION

HUMAN NUCLEIC ACID SEQUENCES FROM HYSTEROMYOMIC TISSUE

APPLICANT(S) FOR DO/EO/US


SPECHT, Thomas, et al.

**Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:**

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371.
- ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
- ☒ A proper Demand for International Preliminary Examination was made by the 19<sup>th</sup> month from the earliest claimed priority date.
- ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
  - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
  - b. ☒ has been transmitted by the International Bureau.
  - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☒ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
7. ☐ A copy of the International Search Report (PCT/ISA/210).
8. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
  - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
  - b. ☐ have been transmitted by the International Bureau.
  - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
  - d. ☒ have not been made and will not be made.
9. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
10. ☐ An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
11. ☐ A copy of the International Preliminary Examination Report (PCT/IPEA/409).
12. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).

**Items 13. to 19. below concern document(s) or information included:**

13. ☐ An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
14. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included.
15. ☒ A FIRST preliminary amendment.
  - ☐ A SECOND or SUBSEQUENT preliminary amendment.
16. ☐ A substitute specification.
17. ☐ A change of power of attorney and/or address letter.
18. ☐ Certificate of Mailing by Express Mail
19. ☐ Other items or information:

U.S. APPLICATION NO. <b>09/673400</b>		INTERNATIONAL APPLICATION NO. <b>PCT/DE99/01178</b>		ATTORNEY'S DOCKET NUMBER <b>SCH 1779</b>	
<input checked="" type="checkbox"/> The following fees are submitted:				<b>CALCULATIONS</b> PTO USE ONLY	
<b>17. BASIC NATIONAL FEE ( 37 CFR §1.492 (a) (1) - (5)):</b>					
Search Report has been prepared by the EPO or JPO.....				\$860.00	
International preliminary examination fee paid to USPTO (37 CFR §1.482).....				\$690.00	
No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2)).....				\$710.00	
Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO.....				\$1,000.00	
International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4).....				\$100.00	
<b>ENTER APPROPRIATE BASIC FEE AMOUNT =</b>				<b>\$860.00</b>	
Surcharge of <b>\$130.00</b> for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30				<b>\$0.00</b>	
<b>CLAIMS</b>		<b>NUMBER FILED</b>	<b>NUMBER EXTRA</b>	<b>RATE</b>	
Total claims		38 - 20 =	18	x \$ 18.00	\$324.00
Independent claims		6 - 3 =	3	x \$ 80.00	\$240.00
MULTIPLE DEPENDENT CLAIM(S) (if applicable)				+ \$ 270.00	
<b>TOTAL OF ABOVE CALCULATIONS =</b>				<b>\$1,424.00</b>	
Reduction of ½ for filing by small entity, if applicable. A Verified Small Entity Statement must also be filed (Note 37 C.F.R. §§1.9, 1.27, 1.28).					
<b>SUBTOTAL =</b>				<b>\$1,424.00</b>	
Processing fee of <b>\$130.00</b> for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
<b>TOTAL NATIONAL FEE =</b>				<b>\$1,424.00</b>	
Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property.					
<b>TOTAL FEES ENCLOSED =</b>				<b>\$1,424.00</b>	
				Amount to be refunded:	
				charged:	
a. <input checked="" type="checkbox"/> A check in the amount of <u>\$1,424.00</u> to cover the above fees is enclosed.					
b. <input type="checkbox"/> Please charge my Deposit Account No. <u>13-3402</u> in the amount of \$_____ to cover the above fees. A duplicate copy of this sheet is enclosed.					
c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>13-3402</u> . A duplicate copy of this sheet is enclosed.					
<b>NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.137(a) or (b)) must be filed and granted to restore the application to pending status.</b>					
SEND ALL CORRESPONDENCE TO:					
MILLEN, WHITE, ZELANO & BRANIGAN, P.C. Arlington Courthouse Plaza I 2200 Clarendon Boulevard, Suite 1400 Arlington, Virginia 22201 (703) 243-6333					
Filed: October 17, 2000				SIGNATURE 	
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				REGISTRATION NUMBER <u>27,969</u>	

**IN THE UNITED STATES DESIGNATED/ELECTED OFFICE**

International Application No. : PCT/DE99/01178  
International Filing Date : 15 April 1999  
Priority Date(s) Claimed : 17 April 1998  
Applicant(s) (DO/EO/US) : SPECHT, Thomas, et al.

Title: HUMAN NUCLEIC ACID SEQUENCES FROM HYSTEROMYOMIC TISSUE

**PRELIMINARY AMENDMENT**

Commissioner for Patents  
Washington, D.C. 20231

Sir:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend this application as follows:

**IN THE CLAIMS:**

Claims 5 and 6, line 1: Change "claims 1 to 4" to -- claim 3 --.

Claim 7: Please rewrite as follows:

7. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claim[s 1 to 6]3, in such a sufficient amount that they hybridize with the sequences [according to claims 1 to 6] of claim 3 or a sequence having 90% homology thereto.

Claims 8 and 9, line 1: Change "claims 1 to 7" to -- claim 3 --.

Claim 10, lines 1 and 2: Change "claims 1 to 9" to -- claim 3 --.

Claim 11, line 2: Change "claims 1 to 9" to -- claim 3 --.

Claim 13, lines 1 and 2: Change "claims 11 and 12" to -- claim 11 --.

Claim 14, lines 1 and 2: Change "claims 1 to 10" to -- claim 3 --.

Claim 16, line 3: Change "claims 1 to 10" to -- claim 3 --.

Claim 18, line 1: Change "claims 16 or 17" to -- claim 16 --.

Claim 19, line 2: Change "claims 16 to 18" to -- claim 16 --.

Claim 27, line 2: After "53-55" insert -- of claim 23 --.

Claim 28, line 2: After "52" insert -- of claim 3 --.  
Claim 29, line 2: After "52" insert -- of claim 3 --.  
Claims 30 and 31, line 2: After "53-55" insert -- of claim 23 --.  
Claim 32, line 3: After "53-55" insert -- of claim 23 --.  
Claims 33 and 34, line 1: Change "claims 1 to 10" to -- claim 3 --.  
Claim 35 line 4: After "52" insert -- of claim 3 --.  
Claim 38, line 1: Change "claims 1 to 7" to -- claim 3 --.

### Remarks

The purpose of this Preliminary Amendment is to eliminate multiple and improper multiple dependent claims to avoid additional fees. Applicants reserve the right to reintroduce claims directed to canceled combined subject matter.

Respectfully submitted,

  
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(54) **Title: HUMAN NUCLEIC ACID SEQUENCES FROM HYSTEROMYOMIC  
TISSUE**

(57) **Abstract**

Human nucleic acid sequences -- mRNA, cDNA, genomic  
sequences -- from hysteryomyomic tissue, which code for gene  
products or portions thereof, and their use, are described. In  
addition, the polypeptides that can be obtained by way of the  
sequences and their use are described.

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### Human Nucleic Acid Sequences from Hysteromyomic Tissue

The invention relates to human nucleic acid sequences from hysteromyomic tissue, which code for gene products or portions thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death by cancer in women is hysteromyoma, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

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A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer ( $> 2000$  nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this possibility of error can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52, which play a role as candidate genes in the hysteryoma, have now been found.

Nucleic acid sequences Seq. ID Nos. 14-18, 30, 31 and 52 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a portion thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 14-18, 30, 31 and 52.
- b) an allelic variation of the nucleic acid sequences named under a)
- or
- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 14-18, 30, 31 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

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The invention also relates to nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52, which are expressed elevated in the hystero myoma.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 14-18, 30, 31 and 52.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 14-18, 30, 31 and 52 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs,  $\phi$ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia),
2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

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Control or regulatory sequences are defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

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The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides, according to the sequence protocols ORF ID Nos. 32-51 and ORF ID Nos. 53-55.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of ORF ID Nos. 32-51 and ORF ID Nos. 53-55 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-31 and Seq. ID No. 52 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide

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partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The polypeptides of sequences Seq. ID Nos. 32-51 and Seq. ID Nos. 53-55 according to the invention can also be used as tools for finding active ingredients against hystero myoma, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52 for expression of polypeptides, which can be used as tools for finding active ingredients against hystero myoma.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID No. 32 to Seq. ID No. 51 and Seq. ID Nos. 53-55 as pharmaceutical agents in the gene therapy for treatment of hystero myoma or for the production of a pharmaceutical agent for treatment of hystero myoma.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 32 to 51 and Seq. ID Nos. 53-55.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID Nos. 1-31, and 52, and their use

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together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences) Seq. ID Nos. 1-31 and 52, genomic BAC, PAC and cosmid libraries are screened, and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes, and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-31 and 52, for use as vehicles for gene transfer.

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## Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes)

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus)

Singleton = A contig that contains only one sequence

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins

N = selectively the nucleotide A, T, G or C

X = selectively one of the 20 naturally occurring amino acids

## Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

## Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

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- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

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### Example 1

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.



Figures 2b1-2b4 illustrate the lengthening of the hysteryomyomic tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another.)

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

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## Example 2

### Algorithm for Identification and Lengthening of Partial cDNA Sequences with Altered Expression Pattern

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

#### 2.1. Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

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**2.1.1**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 30 was found, which occurs more frequently in the hysterymyomic tissue than in normal tissue.

The result is as follows:

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529 Rec'd PCT/PTC 17 OCT 2000

Electronic Northern for SEQ. ID NO.: 30

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0109	0.0021	5.1181	0.1954
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0340	0.0000	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

00/222T 004E/960

**2.1.2.**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 31 was found, which occurs more frequently in the hysteryomyomic tissue than in normal tissue.

The result is as follows:

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Electronic Northern for SEQ. ID NO.: 31

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0051	0.0000 undef	
Small intestine	0.0038	0.0019	2.0416 0.4898	
Ovary	0.0031	0.0000	undef 0.0000	
Endocrine tissue	0.0030	0.0104	0.2878 3.4745	
Gastrointestinal	0.0034	0.0100	0.3396 2.9444	
Brain	0.0057	0.0046	1.2425 0.8048	
Hematopoietic	0.0111	0.0051	2.1599 0.4630	
Skin	0.0040	0.0000	undef 0.0000	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0048	0.0000	undef 0.0000	
Testicles	0.0095	0.0000	undef 0.0000	
Lung	0.0058	0.0000	undef 0.0000	
Stomach-esophagus	0.0042	0.0102	0.4064 2.4605	
Muscle-skeleton	0.0000	0.0000	undef undef	
Kidney	0.0034	0.0060	0.5711 1.7510	
Pancreas	0.0163	0.0068	2.3791 0.4203	
Penis	0.0017	0.0000	undef 0.0000	
Prostate	0.0090	0.0000	undef 0.0000	
Uterus-endometrium	0.0022	0.0021	1.0236 0.9769	
Uterus-myometrium	0.0135	0.0000	undef 0.0000	
Uterus-general	0.0000	0.0340	0.0000 undef	
Breast hyperplasia	0.0000	0.0000	undef undef	
Prostate hyperplasia	0.0224			
Seminal vesicle	0.0030			
Sensory organs	0.0089			
White blood cells	0.0000			
Cervix	0.0061			
	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0254	Lung	0.0082
Placenta	0.0062	Nerves	0.0000
Prostate	0.0303	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0126	Uterus_n	0.0000

004221-004E2960

Electronic Northern for SEQ. ID NO.: 1

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0204
Ovary_n	0.1395
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0256
Gastrointestinal	0.0488
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles	0.0154
Lung	0.0082
Nerves	0.0191
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0000

## Electronic Northern for SEQ. ID NO.: 2

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0102	0.3814	2.6222
Small intestine	0.0128	0.0038	3.4026	0.2939
Ovary	0.0031	0.0165	0.1854	5.3946
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0017	0.0075	0.2264	4.4166
Brain	0.0019	0.0093	0.2071	4.8289
Hematopoietic	0.0022	0.0103	0.2160	4.6299
Skin	0.0040	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0011	0.0137	0.0771	12.9706
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0021	0.0082	0.2540	3.9367
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0120	0.0000	undef
Pancreas	0.0054	0.0000	undef	0.0000
Penis	0.0000	0.0055	0.0000	undef
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0021	0.0000	undef
Uterus-myometrium	0.0000	0.0528	0.0000	undef
Uterus-general	0.0000	0.0408	0.0000	undef
Breast hyperplasia	0.0051	0.0954	0.0534	18.7357
Prostate hyperplasia	0.0064			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
% frequency

Development	
Gastrointestinal	0.0974
Brain	0.0333
Hematopoietic	0.0063
Skin	0.0157
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0249
Suprarenal gland	0.0325
Kidney	0.0761
Placenta	0.0618
Prostate	0.0727
Sensory organs	0.0249
	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0384
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0259
Testicles	0.0000
Lung	0.0328
Nerves	0.0171
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0083

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## Electronic Northern for SEQ. ID NO.: 3

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.1103	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0140	0.0010	13.6792	0.0731
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0815	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

Development	
Gastrointestinal	0.0000
Brain	0.0028
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0090
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0000

002221 00487960

Electronic Northern for SEQ. ID NO.: 4

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0031	0.0165	0.1954	5.3946
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0007	0.0031	0.2400	4.1669
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.1695	0.0000	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0095	0.0412	0.2313	4.3235
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0041	0.5080	1.9684
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0120	0.1428	7.0040
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0883	0.1727	5.7919
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development  
Gastrointestinal  
Brain  
Hematopoietic  
Skin  
Hepatic  
Heart-blood vessels  
Lung  
Suprarenal gland  
Kidney  
Placenta  
Prostate  
Sensory organs

0.0278  
0.0139  
0.0000  
0.0000  
0.0000  
0.0000  
0.0213  
0.0253  
0.0000  
0.0185  
0.0061  
0.0000  
0.0000

Breast  
Ovary\_n  
Ovary\_t  
Endocrine tissue  
Fetal  
Gastrointestinal  
Hematopoietic  
Skin-muscle  
Testicles  
Lung  
Nerves  
Prostate  
Sensory Organs  
Uterus\_n

0.0068  
0.0000  
0.0000  
0.0000  
0.0093  
0.0122  
0.0000  
0.0130  
0.0000  
0.0000  
0.0000  
0.0000  
0.0000  
0.0000

00673400-122700

Electronic Northern for SEQ. ID NO.: 5

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0390	0.0332	1.1734	0.8522
Small intestine	0.0345	0.0414	0.8352	1.1973
Ovary	0.0399	0.0662	0.6024	1.6599
Endocrine tissue	0.0359	0.0546	0.6579	1.5201
Gastrointestinal	0.0528	0.0351	1.5040	0.6649
Brain	0.0172	0.0185	0.9319	1.0731
Hematopoietic	0.0214	0.0359	0.5965	1.6763
Skin	0.0294	0.0379	0.7763	1.2881
Hepatic	0.0257	0.1695	0.1516	6.5954
Heart	0.0476	0.0323	1.4706	0.6800
Testicles	0.0276	0.0000	undef	0.0000
Lung	0.0633	0.0234	2.7059	0.3696
Stomach-esophagus	0.0312	0.0266	1.1724	0.8530
Muscle-skeleton	0.0387	0.0153	2.5211	0.3967
Kidney	0.0308	0.0360	0.8567	1.1673
Pancreas	0.0326	0.0548	0.5948	1.6813
Penis	0.0132	0.0221	0.5983	1.6714
Prostate	0.0479	0.0000	undef	0.0000
Uterus-endometrium	0.0153	0.0319	0.4777	2.0934
Uterus-myometrium	0.0473	0.0528	0.8962	1.1158
Uterus-general	0.0305	0.1019	0.2993	3.3415
Breast hyperplasia	0.0560	0.1908	0.2936	3.4065
Prostate hyperplasia	0.0448			
Seminal vesicle	0.0446			
Sensory organs	0.1513			
White blood cells	0.0235			
Cervix	0.0061			
	0.0426			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0136
Gastrointestinal	0.0974	Ovary_n	0.0000
Brain	0.0222	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0197	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0356	Skin-muscle	0.0324
Suprarenal gland	0.0325	Testicles	0.0231
Kidney	0.0000	Lung	0.0328
Placenta	0.0185	Nerves	0.0131
Prostate	0.0909	Prostate	0.0068
Sensory organs	0.1496	Sensory Organs	0.0077
	0.0126	Uterus_n	0.0208

004222T 004E7950

Electronic Northern for SEQ. ID NO.: 6

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0429	0.1278	0.3356	2.9798
Small intestine	0.1036	0.1203	0.8613	1.1610
Ovary	0.0215	0.0992	0.2163	4.6240
Endocrine tissue	0.0599	0.0702	0.8528	1.1726
Gastrointestinal	0.0783	0.0426	1.8380	0.5441
Brain	0.0249	0.0786	0.3167	3.1574
Hematopoietic	0.0429	0.1284	0.3341	2.9935
Skin	0.0227	0.1136	0.2000	5.0008
Hepatic	0.0844	0.1695	0.4982	2.0073
Heart	0.0523	0.0712	0.7353	1.3600
Testicles	0.0922	0.1649	0.5590	1.7890
Lung	0.0460	0.0585	0.7872	1.2704
Stomach-esophagus	0.0447	0.0797	0.5601	1.7853
Muscle-skeleton	0.0000	0.0537	0.0000	undef
Kidney	0.1490	0.1380	1.0801	0.9258
Pancreas	0.0489	0.0479	1.0196	0.9808
Penis	0.0149	0.1049	0.1417	7.0571
Prostate	0.0509	0.1333	0.3819	2.6187
Uterus-endometrium	0.0196	0.0319	0.6142	1.6282
Uterus-myometrium	0.0676	0.1583	0.4268	2.3432
Uterus-general	0.0381	0.3260	0.1169	8.5541
Breast hyperplasia	0.0560	0.0000	undef	0.0000
Prostate hyperplasia	0.0863			
Seminal vesicle	0.0297			
Sensory organs	0.0089			
White blood cells	0.0353			
Cervix	0.0078			
	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development  
Gastrointestinal  
Brain  
Hematopoietic  
Skin  
Hepatic  
Heart-blood vessels  
Lung  
Suprarenal gland  
Kidney  
Placenta  
Prostate  
Sensory organs

0.1670  
0.1444  
0.0125  
0.0629  
0.0000  
0.0000  
0.0889  
0.0759  
0.2535  
0.1112  
0.1091  
0.1247  
0.1004

Breast  
Ovary\_n  
Ovary\_t  
Endocrine tissue  
Fetal  
Gastrointestinal  
Hematopoietic  
Skin-muscle  
Testicles  
Lung  
Nerves  
Prostate  
Sensory Organs  
Uterus\_n

0.0476  
0.1595  
0.0203  
0.0000  
0.0379  
0.0122  
0.0000  
0.0486  
0.0077  
0.0164  
0.0251  
0.0068  
0.0155  
0.0167

00673400.123700

## Electronic Northern for SEQ. ID NO.: 7

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0051	2.2882	0.4370
Breast	0.0128	0.0075	1.7013	0.5878
Small intestine	0.0153	0.0331	0.4634	2.1579
Ovary	0.0150	0.0104	1.4391	0.6949
Endocrine tissue	0.0085	0.0050	1.6981	0.5889
Gastrointestinal	0.0096	0.0278	0.3451	2.8974
Brain	0.0059	0.0113	0.5236	1.9098
Hematopoietic	0.0254	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0143	0.0194	0.7353	1.3600
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0058	0.0234	0.2460	4.0652
Lung	0.0104	0.0245	0.4234	2.3620
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0360	0.1428	7.0040
Kidney	0.0244	0.0068	3.5687	0.2802
Pancreas	0.0083	0.0000	undef	0.0000
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0218	0.0064	3.4121	0.2931
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0408	0.0000	undef
Uterus-general	0.0192	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0235			
Sensory organs	0.0208			
White blood cells	0.0213			
Cervix				

FETUS  
% frequency

Development	
Gastrointestinal	0.0278
Brain	0.0083
Hematopoietic	0.0125
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0071
Suprarenal gland	0.0036
Kidney	0.0000
Placenta	0.0309
Prostate	0.0061
Sensory organs	0.0249
	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0245
Fetal	0.0093
Gastrointestinal	0.0122
Hematopoietic	0.0342
Skin-muscle	0.0097
Testicles	0.0154
Lung	0.0082
Nerves	0.0080
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0042

002221 00484960

Electronic Northern for SEQ. ID NO.: 8

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0460	0.6780	1.4750
Breast	0.0192	0.0282	0.6805	1.4694
Small intestine	0.0368	0.0000	undef	0.0000
Ovary	0.0210	0.0364	0.5756	1.7372
Endocrine tissue	0.0290	0.0326	0.8882	1.1258
Gastrointestinal	0.0460	0.0231	1.9880	0.5030
Brain	0.0532	0.0585	0.9094	1.0996
Hematopoietic	0.0361	0.0379	0.9528	1.0496
Skin	0.0367	0.0000	undef	0.0000
Hepatic	0.0048	0.0647	0.0735	13.5999
Heart	0.0699	0.0412	1.6961	0.5896
Testicles	0.0288	0.4210	0.0683	14.6349
Lung	0.0343	0.0368	0.9314	1.0737
Stomach-esophagus	0.0773	0.0230	3.3614	0.2975
Muscle-skeleton	0.0497	0.0660	0.7528	1.3283
Kidney	0.0353	0.1575	0.2241	4.4619
Pancreas	0.0165	0.0939	0.1760	5.6828
Penis	0.0299	0.0267	1.1232	0.8903
Prostate	0.0196	0.0298	0.6580	1.5197
Uterus-endometrium	0.0270	0.1583	0.1707	5.8579
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0505			
Seminal vesicle	0.0890			
Sensory organs	0.0353			
White blood cells	0.0399			
Cervix	0.0319			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development  
Gastrointestinal  
Brain  
Hematopoietic  
Skin  
Hepatic  
Heart-blood vessels  
Lung  
Suprarenal gland  
Kidney  
Placenta  
Prostate  
Sensory organs

0.0417  
0.0333  
0.0313  
0.0197  
0.0000  
0.0000  
0.0783  
0.0217  
0.0507  
0.0309  
0.0727  
0.0997  
0.0000

Breast  
Ovary\_n  
Ovary\_t  
Endocrine tissue  
Fetal  
Gastrointestinal  
Hematopoietic  
Skin-muscle  
Testicles  
Lung  
Nerves  
Prostate  
Sensory Organs  
Uterus\_n

0.0000  
0.0000  
0.0152  
0.0000  
0.0082  
0.0244  
0.0057  
0.0032  
0.0077  
0.0082  
0.0141  
0.0000  
0.0310  
0.0125

002227 00422950

## Electronic Northern for SEQ. ID NO.: 9

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0468	0.0204	2.2882	0.4370
Breast	0.0205	0.0451	0.4537	2.2042
Small intestine	0.0307	0.0331	0.9268	1.0789
Ovary	0.0539	0.0468	1.1513	0.8686
Endocrine tissue	0.0562	0.0527	1.0674	0.9369
Gastrointestinal	0.0249	0.0324	0.7692	1.3001
Brain	0.0333	0.0318	1.0451	0.9568
Hematopoietic	0.0388	0.0379	1.0234	0.9772
Skin	0.0257	0.1695	0.1516	6.5954
Hepatic	0.0095	0.0259	0.3676	2.7200
Heart	0.0540	0.0000	undef	0.0000
Testicles	0.0173	0.0702	0.2460	4.0652
Lung	0.0291	0.0491	0.5927	1.6872
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0206	0.1140	0.1803	5.5448
Kidney	0.0733	0.0274	2.6765	0.3736
Pancreas	0.0264	0.0331	0.7977	1.2536
Penis	0.0269	0.0533	0.5054	1.9786
Prostate	0.0501	0.0341	1.4715	0.6796
Uterus-endometrium	0.0541	0.2639	0.2049	4.8816
Uterus-myometrium	0.0132	0.0611	0.2494	4.0097
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0512			
Prostate hyperplasia	0.0386			
Seminal vesicle	0.0623			
Sensory organs	0.0470			
White blood cells	0.0286			
Cervix	0.0426			

FETUS  
% frequency

Development	
Gastrointestinal	0.0557
Brain	0.0666
Hematopoietic	0.0626
Skin	0.0786
Hepatic	0.0000
Heart-blood vessels	0.0260
Lung	0.0818
Suprarenal gland	0.0867
Kidney	0.0761
Placenta	0.0432
Prostate	0.0606
Sensory organs	0.0249
	0.0629

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0068
Ovary_n	0.1595
Ovary_t	0.0051
Endocrine tissue	0.0245
Fetal	0.0256
Gastrointestinal	0.0732
Hematopoietic	0.0057
Skin-muscle	0.0551
Testicles	0.0309
Lung	0.0737
Nerves	0.0231
Prostate	0.0137
Sensory Organs	0.0310
Uterus_n	0.0333

00222T 004E2950

## Electronic Northern for SEQ. ID NO.: 10

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1131	0.1431	0.7900	1.2659
Breast	0.1356	0.1692	0.8015	1.2476
Small intestine	0.1962	0.0165	11.8636	0.0843
Ovary	0.1827	0.2446	0.7471	1.3385
Endocrine tissue	0.1090	0.1329	0.8202	1.2192
Gastrointestinal	0.1878	0.2590	0.7248	1.3797
Brain	0.1035	0.1325	0.7814	1.2798
Hematopoietic	0.2700	0.1894	1.4257	0.7014
Skin	0.1358	0.0847	1.6028	0.6239
Hepatic	0.0428	0.1812	0.2363	4.2311
Heart	0.2586	0.0137	18.8118	0.0532
Testicles	0.0633	0.1403	0.4510	2.2174
Lung	0.3231	0.2229	1.4495	0.6899
Stomach-esophagus	0.1643	0.2147	0.7653	1.3066
Muscle-skeleton	0.1970	0.0960	2.0524	0.4872
Kidney	0.1222	0.2328	0.5248	1.9055
Pancreas	0.0876	0.1767	0.4955	2.0183
Penis	0.1407	0.1600	0.8798	1.1366
Prostate	0.1003	0.0766	1.3080	0.7645
Uterus-endometrium	0.1824	0.0528	3.4569	0.2893
Uterus-myometrium	0.1677	0.3804	0.4409	2.2681
Uterus-general	0.2292	0.0000	undef	0.0000
Breast hyperplasia	0.0735			
Prostate hyperplasia	0.0684			
Seminal vesicle	0.1335			
Sensory organs	0.0470			
White blood cells	0.2749			
Cervix	0.0958			

FETUS  
% frequency

Development	
Gastrointestinal	0.0139
Brain	0.0639
Hematopoietic	0.1063
Skin	0.1258
Hepatic	0.2513
Heart-blood vessels	0.0260
Lung	0.0712
Suprarenal gland	0.1517
Kidney	0.0000
Placenta	0.0988
Prostate	0.0909
Sensory organs	0.1745
	0.0377

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0136
Ovary_n	0.3190
Ovary_t	0.0709
Endocrine tissue	0.0000
Fetal	0.0326
Gastrointestinal	0.1464
Hematopoietic	0.0000
Skin-muscle	0.1328
Testicles	0.0154
Lung	0.2211
Nerves	0.0311
Prostate	0.0410
Sensory Organs	0.0000
Uterus_n	0.0333

002221 004E2950



## Electronic Northern for SEQ. ID NO.: 11

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0136	0.0051	3.0509	0.3278
Small intestine	0.0064	0.0113	0.5671	1.7633
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0240	0.0234	1.0233	0.9772
Gastrointestinal	0.0068	0.0100	0.6792	1.4722
Brain	0.0096	0.0046	2.0708	0.4829
Hematopoietic	0.0022	0.0257	0.0864	11.5747
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0238	0.0065	3.6765	0.2720
Testicles	0.0276	0.0275	1.0023	0.9977
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0083	0.0245	0.3387	2.9526
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0086	0.0060	1.4278	0.7004
Pancreas	0.0081	0.0616	0.1322	7.5658
Penis	0.0165	0.0000	undef	0.0000
Prostate	0.0120	0.0267	0.4493	2.2259
Uterus-endometrium	0.0065	0.0085	0.7677	1.3026
Uterus-myometrium	0.0270	0.0000	undef	0.0000
Uterus-general	0.0076	0.0951	0.0802	12.4748
Breast hyperplasia	0.0968	0.0000	undef	0.0000
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0089			
Sensory organs	0.0089			
White blood cells	0.0706			
Cervix	0.0000			
	0.0106			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development  
Gastrointestinal  
Brain  
Hematopoietic  
Skin  
Hepatic  
Heart-blood vessels  
Lung  
Suprarenal gland  
Kidney  
Placenta  
Prostate  
Sensory organs

0.0139  
0.0278  
0.0000  
0.0708  
0.0000  
0.0000  
0.0320  
0.0036  
0.0000  
0.0124  
0.2121  
0.0000  
0.0000

Breast  
Ovary\_n  
Ovary\_t  
Endocrine tissue  
Fetal  
Gastrointestinal  
Hematopoietic  
Skin-muscle  
Testicles  
Lung  
Nerves  
Prostate  
Sensory Organs  
Uterus\_n

0.0000  
0.0000  
0.0000  
0.0000  
0.0233  
0.0244  
0.0000  
0.0648  
0.0000  
0.0164  
0.0010  
0.0068  
0.0000  
0.0083

002221 0042960

## Electronic Northern for SEQ. ID NO.: 12

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0351	0.3093	0.1135	8.8135
Breast	0.0269	0.0470	0.5716	1.7493
Small intestine	0.0092	0.0662	0.1390	7.1929
Ovary	0.0569	0.0182	3.1248	0.3200
Endocrine tissue	0.0528	0.0502	1.0528	0.9498
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0022	0.0873	0.0254	39.3541
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0220	0.5085	0.0433	23.0839
Hepatic	0.0285	0.0582	0.4902	2.0400
Heart	0.0191	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0114	0.0061	1.8628	0.5368
Stomach-esophagus	0.0193	0.0077	2.5211	0.3967
Muscle-skeleton	0.0771	0.0540	1.4278	0.7004
Kidney	0.0489	0.0137	3.5687	0.2802
Pancreas	0.0264	0.0442	0.5983	1.6714
Penis	0.0090	0.1066	0.0842	11.8713
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0743	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.1494	0.2551	3.9206
Uterus-general	0.0153	0.0954	0.1601	6.2452
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

Development	
Gastrointestinal	0.0696
Brain	0.4387
Hematopoietic	0.0000
Skin	0.2713
Hepatic	0.0000
Heart-blood vessels	1.6121
Lung	0.0605
Suprarenal gland	0.1770
Kidney	1.1663
Placenta	0.8092
Prostate	0.7635
Sensory organs	0.0499
	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0612
Ovary_n	0.0000
Ovary_t	0.1114
Endocrine tissue	0.0000
Fetal	0.4665
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0030
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0291

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## Electronic Northern for SEQ. ID NO.: 13

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0078	0.0204	0.3814	2.6222
Small intestine	0.0256	0.0432	0.5918	1.6899
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0060	0.0078	0.7675	1.3029
Gastrointestinal	0.0000	0.0050	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0074	0.0216	0.3428	2.9168
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0115	0.0468	0.2460	4.0652
Stomach-esophagus	0.0031	0.0082	0.3810	2.6245
Muscle-skeleton	0.0580	0.0000	undef	0.0000
Kidney	0.0000	0.0300	0.0000	undef
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0033	0.0276	0.1197	8.3571
Prostate	0.0210	0.1066	0.1966	5.0877
Uterus-endometrium	0.0022	0.0043	0.5118	1.9538
Uterus-myometrium	0.0135	0.0000	undef	0.0000
Uterus-general	0.0305	0.0883	0.3453	2.8959
Breast hyperplasia	0.0102	0.0000	undef	0.0000
Prostate hyperplasia	0.0160			
Seminal vesicle	0.0059			
Sensory organs	0.0356			
White blood cells	0.0000			
Cervix	0.0035			
	0.0639			

FETUS  
% frequency

Development	
Gastrointestinal	0.0000
Brain	0.0028
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0145
Kidney	0.0761
Placenta	0.0247
Prostate	0.0061
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0408
Ovary_n	0.0000
Ovary_t	0.1266
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0000
Nerves	0.0030
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0208

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## Electronic Northern for SEQ. ID NO.: 14

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0195	0.0051	3.8136	0.2622
Small intestine	0.0051	0.0132	0.3889	2.5715
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0150	0.0130	1.1513	0.8686
Gastrointestinal	0.0153	0.0150	1.0189	0.9815
Brain	0.0115	0.0000	undef	0.0000
Hematopoietic	0.0133	0.0133	0.9969	1.0031
Skin	0.0174	0.0000	undef	0.0000
Hepatic	0.0147	0.0000	undef	0.0000
Heart	0.0000	0.0194	0.0000	undef
Testicles	0.0265	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0042	0.0164	0.2540	3.9367
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0069	0.0540	0.1269	7.8795
Pancreas	0.0217	0.0274	0.7930	1.2610
Penis	0.0165	0.0055	2.9915	0.3343
Prostate	0.0090	0.0000	undef	0.0000
Uterus-endometrium	0.0087	0.0170	0.5118	1.9538
Uterus-myometrium	0.0338	0.2111	0.1600	6.2484
Uterus-general	0.0076	0.0475	0.1603	6.2374
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0320			
Seminal vesicle	0.0238			
Sensory organs	0.0267			
White blood cells	0.0000			
Cervix	0.0069			
	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0417	Ovary_n	0.0068
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0051
Skin	0.0157	Fetal	0.0245
Hepatic	0.0000	Gastrointestinal	0.0035
Heart-blood vessels	0.0000	Hematopoietic	0.0244
Lung	0.0427	Skin-muscle	0.0000
Suprarenal gland	0.0253	Testicles	0.0065
Kidney	0.0000	Lung	0.0000
Placenta	0.0124	Nerves	0.0082
Prostate	0.0121	Prostate	0.0050
Sensory organs	0.0000	Sensory Organs	0.0137
	0.0126	Uterus_n	0.0155
			0.0042

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Electronic Northern for SEQ. ID NO.: 15

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0102	0.7627	1.3111
Breast	0.0026	0.0150	0.1701	5.8778
Small intestine	0.0184	0.0496	0.3707	2.6973
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0007	0.0072	0.1029	9.7228
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0041	0.5080	1.9684
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0086	0.0240	0.3569	2.8016
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0240	0.0000	undef	0.0000
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0096	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0020
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0125
Uterus_n	

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Electronic Northern for SEQ. ID NO.: 16

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0153	0.2542	3.9333
Breast	0.0077	0.0038	2.0416	0.4898
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0119	0.0231	0.4755	2.1032
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0163	0.0246	0.6600	1.5152
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0180	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0135	0.0082	1.6511	0.6057
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0033	0.0276	0.1197	8.3571
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0196	0.0128	1.5354	0.6513
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0408	0.0000	undef
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0375	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0071	Skin-muscle	0.0097
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0507	Lung	0.0082
Placenta	0.0124	Nerves	0.0050
Prostate	0.0061	Prostate	0.0000
Sensory organs	0.0249	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0083

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## Electronic Northern for SEQ. ID NO.: 17

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0307	0.0338	0.9074	1.1021
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0509	0.0286	1.7792	0.5620
Endocrine tissue	0.0375	0.0301	1.2453	0.8030
Gastrointestinal	0.0153	0.0093	1.6567	0.6036
Brain	0.0222	0.0452	0.4909	2.0372
Hematopoietic	0.0160	0.0000	undef	0.0000
Skin	0.0661	0.0000	undef	0.0000
Hepatic	0.0143	0.0518	0.2757	3.6266
Heart	0.0636	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0177	0.0532	0.3322	3.0104
Stomach-esophagus	0.0483	0.0000	undef	0.0000
Muscle-skeleton	0.0137	0.0960	0.1428	7.0040
Kidney	0.0217	0.0685	0.3172	3.1524
Pancreas	0.0264	0.0055	4.7864	0.2089
Penis	0.0449	0.0000	undef	0.0000
Prostate	0.0283	0.0341	0.8317	1.2024
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0671			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0356			
Sensory organs	0.0353			
White blood cells	0.0121			
Cervix	0.0532			

FETUS  
% frequency

Development	0.0557
Gastrointestinal	0.0278
Brain	0.0688
Hematopoietic	0.0275
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0534
Lung	0.0831
Suprarenal gland	0.1014
Kidney	0.0741
Placenta	0.0182
Prostate	0.1247
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0203
Endocrine tissue	0.0490
Fetal	0.0169
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0259
Testicles	0.0000
Lung	0.0082
Nerves	0.0050
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0167

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Electronic Northern for SEQ. ID NO.: 18

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0371	0.0357	1.0387	0.9627
Small intestine	0.0245	0.0331	0.7415	1.3487
Ovary	0.0479	0.0390	1.2280	0.8143
Endocrine tissue	0.0358	0.0326	1.0972	0.9114
Gastrointestinal	0.0153	0.0093	1.6567	0.6036
Brain	0.0229	0.0524	0.4376	2.2851
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0143	0.0518	0.2757	3.6266
Heart	0.0593	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0145	0.0491	0.2964	3.3743
Lung	0.0290	0.0000	undef	0.0000
Stomach-esophagus	0.0120	0.1140	0.1052	9.5055
Muscle-skeleton	0.0299	0.0616	0.4846	2.0634
Kidney	0.0281	0.0055	5.0855	0.1966
Pancreas	0.0449	0.0000	undef	0.0000
Penis	0.0349	0.0319	1.0919	0.9159
Prostate	0.0203	0.0000	undef	0.0000
Uterus-endometrium	0.0152	0.0679	0.2245	4.4553
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0576			
Breast hyperplasia	0.0446			
Prostate hyperplasia	0.0356			
Seminal vesicle	0.0235			
Sensory organs	0.0130			
White blood cells	0.0532			
Cervix				

FETUS  
% frequency

Development	
Gastrointestinal	0.0417
Brain	0.0333
Hematopoietic	0.0688
Skin	0.0275
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0427
Suprarenal gland	0.0867
Kidney	0.1268
Placenta	0.0741
Prostate	0.0182
Sensory organs	0.1247
	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0253
Endocrine tissue	0.0245
Fetal	0.0326
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0518
Testicles	0.0000
Lung	0.0082
Nerves	0.0090
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0208

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## Electronic Northern for SEQ. ID NO.: 19

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0351	0.0332	1.0561	0.9469
Small intestine	0.0269	0.0376	0.7146	1.3995
Ovary	0.0337	0.0992	0.3398	2.9425
Endocrine tissue	0.0240	0.0312	0.7675	1.3029
Gastrointestinal	0.0409	0.0075	5.4340	0.1840
Brain	0.0268	0.0971	0.2761	3.6217
Hematopoietic	0.0059	0.0113	0.5236	1.9098
Skin	0.0013	0.2273	0.0059	170.0273
Hepatic	0.0330	0.0000	undef	0.0000
Heart	0.0095	0.0388	0.2451	4.0800
Testicles	0.0223	0.0000	undef	0.0000
Lung	0.0173	0.0351	0.4920	2.0326
Stomach-esophagus	0.0395	0.0900	0.4388	2.2792
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0857	0.1920	0.4462	2.2413
Pancreas	0.0136	0.0205	0.6609	1.5132
Penis	0.0198	0.0221	0.8974	1.1143
Prostate	0.0629	0.0800	0.7862	1.2719
Uterus-endometrium	0.0087	0.0106	0.8189	1.2211
Uterus-myometrium	0.0676	0.0000	undef	0.0000
Uterus-general	0.0686	0.1630	0.4208	2.3761
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0735			
Seminal vesicle	0.0416			
Sensory organs	0.0000			
White blood cells	0.0235			
Cervix	0.0000			
	0.0426			

FETUS  
% frequency

Development	0.1113
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0289
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.1333
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0204
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0111
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0000
Nerves	0.0068
Prostate	0.0077
Sensory Organs	0.0125
Uterus_n	

00222T 004E2950

Electronic Northern for SEQ. ID NO.: 20

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0858	0.1048	0.8185	1.2217
Breast	0.1036	0.1729	0.5992	1.6690
Small intestine	0.1226	0.1158	1.0593	0.9441
Ovary	0.0958	0.1197	0.8009	1.2486
Endocrine tissue	0.0954	0.1128	0.8453	1.1830
Gastrointestinal	0.0900	0.1573	0.5725	1.7466
Brain	0.0658	0.0924	0.7120	1.4046
Hematopoietic	0.1109	0.0758	1.4645	0.6828
Skin	0.0918	0.0000	undef	0.0000
Hepatic	0.0333	0.0906	0.3676	2.7200
Heart	0.2120	0.0412	5.1398	0.1946
Testicles	0.0690	0.3625	0.1904	5.2509
Lung	0.0696	0.1186	0.5869	1.7040
Stomach-esophagus	0.0483	0.0460	1.0504	0.9520
Muscle-skeleton	0.0702	0.2820	0.2491	4.0145
Kidney	0.0652	0.1027	0.6344	1.5762
Pancreas	0.1140	0.1270	0.8974	1.1143
Penis	0.1018	0.0000	undef	0.0000
Prostate	0.1090	0.1277	0.8530	1.1723
Uterus-endometrium	0.1149	0.0000	undef	0.0000
Uterus-myometrium	0.0686	0.2106	0.3258	3.0692
Uterus-general	0.0458	0.1908	0.2402	4.1635
Breast hyperplasia	0.1279			
Prostate hyperplasia	0.1159			
Seminal vesicle	0.1157			
Sensory organs	0.1059			
White blood cells	0.0832			
Cervix	0.1278			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0136
Gastrointestinal		Ovary_n	0.1595
Brain	0.0557	Ovary_t	0.0658
Hematopoietic	0.2471	Endocrine tissue	0.0000
Skin	0.2189	Fetal	0.0216
Hepatic	0.1612	Gastrointestinal	0.0732
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.1560	Skin-muscle	0.0259
Suprarenal gland	0.2633	Testicles	0.0000
Kidney	0.1012	Lung	0.1638
Placenta	0.1014	Nerves	0.0211
Prostate	0.1112	Prostate	0.0205
Sensory organs	0.0848	Sensory Organs	0.0000
	0.3740	Uterus_n	0.0333
	0.0126		

002221-004E2950

## Electronic Northern for SEQ. ID NO.: 21

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0273	0.0102	2.6695	0.3746
Small intestine	0.0051	0.0019	2.7221	0.3674
Ovary	0.0276	0.0000	undef	0.0000
Endocrine tissue	0.0180	0.0000	undef	0.0000
Gastrointestinal	0.0136	0.0000	undef	0.0000
Brain	0.0134	0.0046	2.8992	0.3449
Hematopoietic	0.0015	0.0164	0.0900	11.1117
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0147	0.0000	undef	0.0000
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0106	0.0412	0.2570	3.8912
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0052	0.0102	0.5080	1.9684
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0223	0.0060	3.7122	0.2694
Pancreas	0.0081	0.0000	undef	0.0000
Penis	0.0033	0.0276	0.1197	8.3571
Prostate	0.0030	0.0267	0.1123	8.9035
Uterus-endometrium	0.0022	0.0043	0.5118	1.9538
Uterus-myometrium	0.0135	0.0000	undef	0.0000
Uterus-general	0.0381	0.1019	0.3741	2.6732
Breast hyperplasia	0.0102	0.0000	undef	0.0000
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0000			
Sensory organs	0.0089			
White blood cells	0.0000			
Cervix	0.0000			
	0.0130			
	0.0106			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0204
Gastrointestinal		Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0111	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0093
Hepatic	0.0157	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0107	Skin-muscle	0.0421
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0247	Nerves	0.0010
Prostate	0.0000	Prostate	0.0274
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0000

002221 004E2950

## Electronic Northern for SEQ. ID NO.: 22

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0102	0.0000	undef
Small intestine	0.0064	0.0207	0.3093	3.2328
Ovary	0.0153	0.0662	0.2317	4.3157
Endocrine tissue	0.0180	0.0156	1.1513	0.8686
Gastrointestinal	0.0204	0.0351	0.5822	1.7176
Brain	0.0153	0.0231	0.6627	1.5090
Hematopoietic	0.0510	0.0257	1.9871	0.5032
Skin	0.0134	0.0000	undef	0.0000
Hepatic	0.0367	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0466	0.0000	undef	0.0000
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0249	0.0348	0.7172	1.3943
Muscle-skeleton	0.0193	0.0077	2.5211	0.3967
Kidney	0.0377	0.0300	1.2564	0.7959
Pancreas	0.0244	0.0274	0.8922	1.1209
Penis	0.0083	0.0166	0.4986	2.0057
Prostate	0.0329	0.0267	1.2355	0.8094
Uterus-endometrium	0.0131	0.0149	0.8774	1.1397
Uterus-myometrium	0.0338	0.0000	undef	0.0000
Uterus-general	0.0000	0.0340	0.0000	undef
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0256			
Seminal vesicle	0.0238			
Sensory organs	0.0000			
White blood cells	0.0069			
Cervix	0.0213			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.3190
Brain	0.0194	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0373
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0320	Skin-muscle	0.0680
Suprarenal gland	0.0434	Testicles	0.0231
Kidney	0.0000	Lung	0.0000
Placenta	0.0124	Nerves	0.0211
Prostate	0.0061	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0077
	0.0251	Uterus_n	0.0458

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Electronic Northern for SEQ. ID NO.: 23				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0741	0.0639	1.1593	0.8626
Breast	0.0691	0.0827	0.8352	1.1973
Small intestine	0.0245	0.0496	0.4943	2.0230
Ovary	0.0689	0.0494	1.3936	0.7176
Endocrine tissue	0.2487	0.5191	0.4791	2.0873
Gastrointestinal	0.0421	0.0879	0.4796	2.0852
Brain	0.1700	0.1037	1.6395	0.6099
Hematopoietic	0.0695	0.0758	0.9175	1.0899
Skin	0.0367	0.4237	0.0866	11.5419
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0668	0.1375	0.4857	2.0588
Testicles	0.0460	0.0468	0.9839	1.0163
Lung	0.0592	0.0470	1.2590	0.7943
Stomach-esophagus	0.1160	0.0690	1.6807	0.5950
Muscle-skeleton	0.0754	0.0960	0.7853	1.2735
Kidney	0.0706	0.0479	1.4728	0.6790
Pancreas	0.0677	0.0552	1.2265	0.8153
Penis	0.0988	0.0267	3.7064	0.2698
Prostate	0.0697	0.0660	1.0566	0.9464
Uterus-endometrium	0.0608	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0611	0.2494	4.0097
Uterus-general	0.1120	0.0000	undef	0.0000
Breast hyperplasia	0.0480	0.0565		
Prostate hyperplasia		0.0445		
Seminal vesicle		0.0823		
Sensory organs		0.0824		
White blood cells		0.0852		
Cervix				

Development		Breast	0.0544
Gastrointestinal	0.1113	Ovary_n	0.0000
Brain	0.0805	Ovary_t	0.0203
Hematopoietic	0.1376	Endocrine tissue	0.0245
Skin	0.1140	Fetal	0.0309
Hepatic	0.0000	Gastrointestinal	0.0610
Heart-blood vessels	0.0520	Hematopoietic	0.0000
Lung	0.0996	Skin-muscle	0.0356
Suprarenal gland	0.1951	Testicles	0.0077
Kidney	0.1268	Lung	0.0655
Placenta	0.1359	Nerves	0.0783
Prostate	0.1030	Prostate	0.0547
Sensory organs	0.0748	Sensory Organs	0.0000
	0.0879	Uterus_n	0.0083

## Electronic Northern for SEQ. ID NO.: 24

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0546	0.0332	1.6428	0.6087
Breast	0.0269	0.0320	0.8407	1.1896
Small intestine	0.0276	0.0000	undef	0.0000
Ovary	0.0479	0.0546	0.8771	1.1401
Endocrine tissue	0.0324	0.0176	1.8437	0.5424
Gastrointestinal	0.0211	0.0463	0.4556	2.1950
Brain	0.0229	0.0277	0.8266	1.2097
Hematopoietic	0.0348	0.0379	0.9175	1.0899
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0190	0.0000	undef	0.0000
Heart	0.0477	0.0000	undef	0.0000
Testicles	0.0230	0.1169	0.1968	5.0816
Lung	0.0156	0.0307	0.5080	1.9684
Stomach-esophagus	0.0000	0.0460	0.0000	undef
Muscle-skeleton	0.0120	0.0480	0.2499	4.0023
Kidney	0.0163	0.0068	2.3791	0.4203
Pancreas	0.0182	0.0331	0.5484	1.8234
Penis	0.0180	0.0800	0.2246	4.4517
Prostate	0.0174	0.0170	1.0236	0.9769
Uterus-endometrium	0.0541	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0576			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0277			
Cervix	0.0213			

FETUS  
% frequency

Development	
Gastrointestinal	0.0278
Brain	0.0639
Hematopoietic	0.0438
Skin	0.0275
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0925
Suprarenal gland	0.0831
Kidney	0.0000
Placenta	0.0803
Prostate	0.0667
Sensory organs	0.0249
	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0077
Lung	0.0000
Nerves	0.0040
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

00673400-12300

Electronic Northern for SEQ. ID NO.: 25

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0429	0.0486	0.8832	1.1323
Breast	0.0435	0.0771	0.5643	1.7720
Small intestine	0.0307	0.0000	undef	0.0000
Ovary	0.0389	0.0833	0.4677	2.1381
Endocrine tissue	0.0460	0.0301	1.5283	0.6543
Gastrointestinal	0.0287	0.0971	0.2958	3.3903
Brain	0.0347	0.0534	0.6507	1.5367
Hematopoietic	0.0869	0.0000	undef	0.0000
Skin	0.0551	0.0847	0.6498	1.5389
Hepatic	0.0143	0.0194	0.7353	1.3600
Heart	0.0466	0.0137	3.3923	0.2948
Testicles	0.0173	0.0935	0.1845	5.4203
Lung	0.0457	0.0613	0.7451	1.3421
Stomach-esophagus	0.0290	0.0153	1.8908	0.5289
Muscle-skeleton	0.0223	0.1140	0.1954	5.1183
Kidney	0.0407	0.0137	2.9739	0.3363
Pancreas	0.0314	0.0442	0.7105	1.4075
Penis	0.0779	0.0533	1.4601	0.6849
Prostate	0.0458	0.0617	0.7412	1.3491
Uterus-endometrium	0.0473	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.1087	0.2806	3.5642
Uterus-general	0.0357	0.0954	0.3736	2.6765
Breast hyperplasia	0.0256			
Prostate hyperplasia	0.0803			
Seminal vesicle	0.0801			
Sensory organs	0.0118			
White blood cells	0.0494			
Cervix	0.0426			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development  
Gastrointestinal  
Brain  
Hematopoietic  
Skin  
Hepatic  
Heart-blood vessels  
Lung  
Suprarenal gland  
Kidney  
Placenta  
Prostate  
Sensory organs

0.0417  
0.0611  
0.0626  
0.0708  
0.0000  
0.0260  
0.0534  
0.0542  
0.0761  
0.0988  
0.0303  
0.0000  
0.0251

Breast  
Ovary\_n  
Ovary\_t  
Endocrine tissue  
Fetal  
Gastrointestinal  
Hematopoietic  
Skin-muscle  
Testicles  
Lung  
Nerves  
Prostate  
Sensory Organs  
Uterus\_n

0.0204  
0.1595  
0.0101  
0.0000  
0.0332  
0.0000  
0.0000  
0.0194  
0.0077  
0.0328  
0.0161  
0.0068  
0.0000  
0.0291

004221 00452950

Electronic Northern for SEQ. ID NO.: 26

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	3.0675	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0340	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal		Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0028	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0061	Prostate	0.0155
Sensory organs	0.0000	Sensory Organs	0.0250
	0.0000	Uterus_n	

00673400-122700



Electronic Northern for SEQ. ID NO.: 27

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0230	0.1695	5.8999
Breast	0.0179	0.0395	0.4537	2.2042
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0300	0.0130	2.3025	0.4343
Endocrine tissue	0.0068	0.0251	0.2717	3.6805
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0015	0.0092	0.1600	6.2504
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0194	0.0000	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0368	0.2258	4.4288
Stomach-esophagus	0.0290	0.0230	1.2605	0.7933
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0136	0.0068	1.9826	0.5044
Pancreas	0.0000	0.0276	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0128	0.5118	1.9538
Uterus-endometrium	0.0473	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0278	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0304
Skin	0.0079	Fetal	0.0245
Hepatic	0.0000	Gastrointestinal	0.0029
Heart-blood vessels	0.0000	Hematopoietic	0.0122
Lung	0.0320	Skin-muscle	0.0114
Suprarenal gland	0.0289	Testicles	0.0097
Kidney	0.0000	Lung	0.0000
Placenta	0.0185	Nerves	0.0164
Prostate	0.0000	Prostate	0.0020
Sensory organs	0.0997	Sensory Organs	0.0068
	0.0000	Uterus_n	0.0000

002221 004E2950

Electronic Northern for SEQ. ID NO.: 28

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0383	0.5085	1.9666
Breast	0.0256	0.0714	0.3582	2.7919
Small intestine	0.0552	0.0331	1.6683	0.5994
Ovary	0.0270	0.0468	0.5756	1.7372
Endocrine tissue	0.0477	0.0431	1.0566	0.9464
Gastrointestinal	0.0326	0.0324	1.0058	0.9942
Brain	0.0503	0.0277	1.8132	0.5515
Hematopoietic	0.0201	0.1894	0.1059	9.4460
Skin	0.0367	0.2542	0.1444	6.9252
Hepatic	0.0476	0.0388	1.2255	0.8160
Heart	0.0699	0.0550	1.2721	0.7861
Testicles	0.0173	0.1403	0.1230	8.1305
Lung	0.0395	0.0818	0.4826	2.0720
Stomach-esophagus	0.0676	0.0613	1.1030	0.9066
Muscle-skeleton	0.0394	0.0300	1.3135	0.7613
Kidney	0.0462	0.0616	0.7490	1.3351
Pancreas	0.0347	0.0607	0.5711	1.7510
Penis	0.0509	0.1600	0.3182	3.1424
Prostate	0.0327	0.0149	2.1935	0.4559
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0543	0.1403	7.1284
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0565			
Seminal vesicle	0.0445			
Sensory organs	0.0941			
White blood cells	0.0390			
Cervix	0.0319			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development  
Gastrointestinal  
Brain  
Hematopoietic  
Skin  
Hepatic  
Heart-blood vessels  
Lung  
Suprarenal gland  
Kidney  
Placenta  
Prostate  
Sensory organs

0.0557  
0.0194  
0.0188  
0.0197  
0.0000  
0.0000  
0.0320  
0.0325  
0.0000  
0.0371  
0.0242  
0.0997  
0.0000

Breast  
Ovary\_n  
Ovary\_t  
Endocrine tissue  
Fetal  
Gastrointestinal  
Hematopoietic  
Skin-muscle  
Testicles  
Lung  
Nerves  
Prostate  
Sensory Organs  
Uterus\_n

0.0340  
0.0000  
0.0101  
0.0000  
0.0396  
0.0244  
0.0000  
0.0778  
0.0000  
0.0000  
0.0231  
0.0479  
0.0697  
0.0291

00422T 004E 2960

## Electronic Northern for SEQ. ID NO.: 29

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0663	0.0358	1.8523	0.5399
Breast	0.0512	0.0489	1.0470	0.9551
Small intestine	0.0368	0.0496	0.7415	1.3487
Ovary	0.0779	0.0728	1.0690	0.9354
Endocrine tissue	0.0562	0.0326	1.7242	0.5800
Gastrointestinal	0.0345	0.0370	0.9319	1.0731
Brain	0.0392	0.0524	0.7482	1.3366
Hematopoietic	0.0602	0.0379	1.5880	0.6297
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0095	0.0647	0.1471	6.7999
Heart	0.0583	0.0550	1.0601	0.9433
Testicles	0.0173	0.1520	0.1135	8.8080
Lung	0.0208	0.0491	0.4234	2.3620
Stomach-esophagus	0.0387	0.0460	0.8404	1.1900
Muscle-skeleton	0.0360	0.0420	0.8567	1.1673
Kidney	0.0380	0.0616	0.6168	1.6213
Pancreas	0.0314	0.0884	0.3552	2.8150
Penis	0.0689	0.0267	2.5833	0.3871
Prostate	0.0436	0.0490	0.8901	1.1235
Uterus-endometrium	0.0541	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.1155	0.3301	3.0296
Uterus-general	0.0815	0.0000	undef	0.0000
Breast hyperplasia	0.0446			
Prostate hyperplasia	0.0801			
Seminal vesicle	0.0353			
Sensory organs	0.0520			
White blood cells	0.0532			
Cervix				

FETUS  
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0389
Hematopoietic	0.0188
Skin	0.0472
Hepatic	0.0000
Heart-blood vessels	0.0260
Lung	0.0498
Suprarenal gland	0.0614
Kidney	0.0254
Placenta	0.0741
Prostate	0.0364
Sensory organs	0.0499
	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.1595
Ovary_t	0.0203
Endocrine tissue	0.0000
Fetal	0.0093
Gastrointestinal	0.0366
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0000
Lung	0.0164
Nerves	0.0120
Prostate	0.0205
Sensory Organs	0.0000
Uterus_n	0.0208

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Electronic Northern for SEQ. ID NO.: 30

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0109	0.0021	5.1181	0.1954
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0340	0.0000	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development  
Gastrointestinal 0.0000  
Brain 0.0000  
Hematopoietic 0.0000  
Skin 0.0000  
Hepatic 0.0000  
Heart-blood vessels 0.0000  
Lung 0.0000  
Suprarenal gland 0.0000  
Kidney 0.0000  
Placenta 0.0000  
Prostate 0.0000  
Sensory organs 0.0000

Breast 0.0000  
Ovary\_n 0.0000  
Ovary\_t 0.0000  
Endocrine tissue 0.0000  
Fetal 0.0000  
Gastrointestinal 0.0000  
Hematopoietic 0.0000  
Skin-muscle 0.0000  
Testicles 0.0000  
Lung 0.0000  
Nerves 0.0068  
Prostate 0.0000  
Sensory Organs 0.0000  
Uterus\_n

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## Electronic Northern for SEQ. ID NO.: 31

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0104	0.2878	3.4745
Endocrine tissue	0.0034	0.0100	0.3396	2.9444
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0111	0.0051	2.1599	0.4630
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0042	0.0102	0.4064	2.4605
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0163	0.0068	2.3791	0.4203
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0224			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0061			
Cervix	0.0213			

FETUS  
% frequency

Development	
Gastrointestinal	0.0000
Brain	0.0028
Hematopoietic	0.0125
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Suprarenal gland	0.0036
Kidney	0.0254
Placenta	0.0062
Prostate	0.0303
Sensory organs	0.0000
	0.0126

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0082
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

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Electronic Northern for Seq. ID: 52

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0599	0.0543	1.1037 0.9060
Large intestine	0.0507	0.0282	1.7979 0.5562
Small intestine	0.0326	0.0450	0.7240 1.3811
Ovary	0.0268	0.0313	0.8563 1.1679
Endocrine tissue	0.0439	0.0426	1.0306 0.9703
Brain	0.0564	0.0453	1.2443 0.8037
Skin	0.0642	0.0530	1.2113 0.8255
Hepatic	0.0380	0.0379	1.0022 0.9978
Heart	0.0330	0.0789	0.4190 2.3868
Testicles	0.0093	0.0508	0.1831 5.4614
Lung	0.0589	0.0000	undef 0.0000
Stomach-esophagus	0.0482	0.0533	0.9047 1.1054
Muscle-skeleton	0.0389	0.0499	0.7796 1.2828
Kidney	0.0072	0.0256	0.2833 3.5296
Pancreas	0.0240	0.0702	0.3418 2.9256
Prostate	0.0694	0.0289	2.3984 0.4169
T lymphoma	0.0297	0.0331	0.8974 1.1143
Uterus	0.0443	0.0287	1.5457 0.6470
White blood cells	0.0505	0.1643	0.3074 3.2533
Hematopoietic	0.0325	0.0690	0.4715 2.1210
Penis	0.0363	0.0304	1.1948 0.8370
Seminal vesicle	0.0495		
Sensory organs	0.0322		
	0.0493		
	0.0470		

FETUS  
% freq.

Development	0.0696
Gastrointestinal	0.0750
Brain	0.0876
Hematopoietic	0.0904
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0854
Lung	0.0867
Adrenal gland	0.0761
Kidney	0.0556
Placenta	0.0606
Prostate	0.0499
Sensory organs	0.0628

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	
Breast t	0.0068
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.1595
Endocrine tissue	0.0101
Fetal	0.0245
Gastrointestinal	0.0284
Hematopoietic	0.0732
Skin-muscle	0.0000
Testicles_n	0.0616
Testicles_t	0.0293
Lungs_n	0.0000
Lungs_t	0.0195
Nerves	0.0000
Kidney t	0.0261
Ovary Uterus	0.0000
Prostate_n	0.0293
Sensory organs	0.0121
White blood cells	0.0310
	0.0000

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## 2.2. Fisher Test

In order to decide whether a partial sequence  $S$  of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to  $S$ . If the null hypothesis can be rejected with high enough certainty, the gene belonging to  $S$  is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

### Example 3

#### Automatic Lengthening of the Partial Sequence

Automatic lengthening of partial sequence  $S$  is completed in three steps:

1. Determination of all sequences homologous to  $S$  from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence  $C$  from the assembled sequences.

Consensus sequence  $C$  will generally be longer than initial sequence  $S$ . Its electronic Northern Blot will accordingly

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deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences  $C_i$  (i: iteration index) obtained in each case until the alternative hypothesis is rejected (if  $H_0$  Exit; truncation criterion I) or until automatic lengthening is no longer possible (while  $C_i > C_{i-1}$ ; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from hysteromyomic tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORF's) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

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**Example 4****Mapping of Nucleic Acid Sequences on the Human Genome**

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server ([http://www.stanford.edu/RH/rhserver\\_form2.html](http://www.stanford.edu/RH/rhserver_form2.html)). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

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the results were evaluated with the above-mentioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

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## TABLE I

Col. 1 - Sequence ID No.:

Col. 2 - Expression in hysteroomyomic tissue:

Col. 3 - Function

Col. 4 - Modules

Col. 5 - Length of the applied sequence in bases

Col. 6 - Cytogenetic localization

Col. 7 - Next marker

[Key to Table I:]

[Col. 2:] erhöht = elevated

[Col. 3:]

[Seq. ID No.: 14, 15, 17, 30, 31] unbekannt = unknown

[Seq. ID No.: 16] Homolog zu Homo sapiens... = homologous  
to homo sapiens...

[Seq. ID No.: 18] Humanes Homolog zu ... = human homolog to

[Seq. ID No.: 52] Verlängerung von Seq. ID. 14 =  
Lengthening of Seq. ID. 14

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TABLE I

Sequenz ID No.:	Expression im Uterus-Myomgewebe:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cyogenetische Lokalisation	nächster Marker
1	erhöht	Human mRNA for ornithine decarboxylase anilizyme	"abhydro-lase"	779		
2	erhöht	Human MEST mRNA		2310		
3	erhöht	Human cocaine and amphetamine regulated transcript CART (hCART)		854	5q11.2-q13.1	D5S1730
4	erhöht	Human microfibril-associated glycoprotein (MFAP2)		1112	1p36.11-p36.13	
5	erhöht	Human mRNA for KIAA0108 gene	"kazal"	1051	2p23.3	D2S387
6	erhöht	Human SPARC/osteonectin	"trm"	1516	5q32-q33.1	
7	erhöht	Homo sapiens splicing factor, arginine/serine-rich 7 (SFRS7)		2367	2p22.3-p22.1	WI-9798
8	erhöht	Human triosephosphate isomerase	3x "TIM"	568		
9	erhöht	Human nuclear ribonucleoprotein particle (hnRNP) C	"Thymosin"	1775		
10	erhöht	Human thymosin beta-4	"IGFBP"	509		
11	erhöht	Human growth hormone-dependent insulin-like growth factor-binding protein mRNA	"thyro-globulin_1"	2191	7p12.2-p13	
12	erhöht	Human H19		1769		
13	erhöht	Human cellular retinoic acid-binding protein II (CRABP)	"lipocalin"	1026		
14	erhöht	unbekannt	"trm"	676	14p11.2-14p11.1	WI-4204
15	erhöht	unbekannt		1254		
16	erhöht	Homolog zu Homo sapiens mRNA for putatively prenylated protein		537		
17	erhöht	unbekannt		823		
18	erhöht	Humanes Homolog zu P. vivax pva1 gene	5x "LRR"	1082		
19	erhöht	Human lumican mRNA	"S2"	1548	12q21.31-12q21.33	D12S351
20	erhöht	Human 37 kD laminin receptor precursor/p40 ribosome associated protein	"pMP22"	844		
21	erhöht	Human YMP		862		
22	erhöht	Human NADH:ubiquinone oxidoreductase MLRQ subunit	"G-alpha", "arf"	546		
23	erhöht	Human mRNA for coupling protein G(s) alpha-subunit	"trm"	1591	20q13.32-q13.33	
24	erhöht	Human hnRNP core protein A1	"HMG14_17"	441		
25	erhöht	Human HMG-17 gene for non-histone chromosomal protein	"hormone"	1131		
26	erhöht	H sapiens mRNA for prolactin (clone PRL205)		1071		
27	erhöht	Human mRNA for neurite outgrowth-promoting protein.	3x "PTN_MK"	896		
28	erhöht	H sapiens mRNA for proliferation-associated gene (pag)	"AtpC-TSA"	1050	1p32.3-p34.3	
29	erhöht	H sapiens alpha NAC		581		
30	erhöht	unbekannt		264		
31	erhöht	unbekannt		111		
52	erhöht	Verlängerung von Seq. ID. 14	"trm"	3665	14p11.2-14p11.1	WI-4204

# References to the modules:

Pfam: Protein families database of alignments and HMMs  
(pfam@sanger.ac.uk)

PROSITE: The PROSITE database, its status in 1999. Nucleic  
Acids Res. 27: 215-219 (<http://www.expasy.ch/sprot/prosite.html>)

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TABLE II

## DNA Sequences

Seq. ID. No.

14

15

16

17

18

30

31

52

## Peptide Sequences (ORF's)

Seq. ID. No.

32

33

34

35

36

37

38

39

40

41

42

43

44

45

46

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The inventive nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 31 of the determined candidate genes and the determined amino acid sequences Seq. ID No. 32 to Seq. ID No. 51 are described in the following sequence protocol.

### Sequence Protocol

#### (1) GENERAL INFORMATION:

##### (i) APPLICANT:

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

##### (ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Hysteromyomic Tissue

##### (iii) Number of sequences: 55

##### (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

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## (2) INFORMATION ON SEQ ID NO. 1:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 779 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

agcgagcagc ggcggcggcg cggagagacg cagcggaggt tttcctgggt tcggacccca 60
gcggccggat ggtgaaatcc tccctgcagc ggatcctcaa tagccactgc ttcgccagag120
agaaggaagg ggataaaacc agcgccacca tccacgccag ccgcaccatg ccgctcctaa180
gcctgcacag ccgcggcggc agcagcagtg agagtccag ggtctccctc cactgctgta240
gtaacccggg tccggggcct cgggtggtgct cctgatgcc ctcacccacc cctgaagatc300
ccaggtgggc gagggaatag tcaaaggac cacaatcttc cagctaactt attctactcc360
gatgatcggc tgaatgtaac agaggaacta acgtccaacg acaagacgag gattctcaac420
gtccagtcca ggctcacaga cgccaaacgc attaactggc gaacagtgct gagtggcggc480
actgctctac atcgagatcc cgggcggcgc gctgcccag gggagcaagg acagctttgc540
agttctcctg ggagttcgct gaggagcagc tgcgaggccg accatgtctt aatttgcttc600
cacaagaacc ccgaggacag agccgccttg ctccgaacct tcagcttttt cgggcttgag660
attttgagac cggggcatcc cctttgttcc ccaagagacc cgacgcttgc ttcatggggc720
tacaagtttc gagagagagt ctttggggag aggaagaagg attaggggcc gcgtcggg 779

```

## (2) INFORMATION ON SEQ ID NO. 2:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2310 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

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## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

gttctccgaa acatggagtc ctgtaggcaa ggtcttacct gaatcaggat gaggagtg 60  
 tgggtccagg tggggctgct ggccgtgccc ctgcttgctg cgtacctgca catcccaccc 120  
 cctcagcgtt cccctgccc tcactcatgg aagtcttcag gcaagttttt cacttacaag 180  
 ggactgcgta tcttctacca agactctgtg ggtgtggttg gaagtccaga gatagttgtg 240  
 cttttacacg gttttccaac atccagctac gactgggtaca agatttgga aggtctgacc 300  
 ttgaggtttc atcgggtgat tgccttgat ttcttaggct ttggcttcag tgacaaaccg 360  
 agaccacatc actattccat atttgagcag gccagcatcg tgggaagcgt tttgcggcat 420  
 ctggggctcc agaaccgcag gatcaacctt ctttctcatg actatggaga tattgttgct 480  
 caggagcttc tctacaggta caagcagaat cgatctggtc ggcttaccat aaagagtctc 540  
 tgtctgtcaa atggaggtat ctttctgag actcacctc cactccttct ccaaaagcta 600  
 ctcaaagatg gaggtgtgct gtcacccatc ctcacacgac tgatgaactt ctttgtattc 660  
 tctcgaggtc tcacccagct ctttgggccc tatactgggc cctctgagag tgagctgttg 720  
 gacatgtggg cagggatccg caacaatgac gggaaacttag tcattgacag tctcttacag 780  
  
 tacatcaatc agaggaagaa gttcagaagg cgctggagg gagctcttgc ctctgtaact 840  
 atccccattc attttatcta tgggccattg gatccca atccctatcc agagtttttg 900  
 gagctgtaca ggaaaacgct gccgcggtcc acagtgaga ttctggatga ccacattagc 960  
 cactatccac agctagagga tcccatgggc ttcttgaatg catatatggg cttcatcaac1020  
 tcttctgag ctggaaagag tagcttccct gtattacctc cctactccc ttatgtgttg1080  
 tgtattccac ttagggaagaa atgccccaaa gaggtcctgg ccatcaaaca taattctctcl140  
 acaaagtcca ctttactcaa attggtgaac agtgtatagg aagaagccag caggagctct1200  
 gactaagggtt gacataatag tccacctccc attactttga tatctgatca aatgtataga1260  
 cttggctttg ttttttgtgc tattaggaaa ttctgatgag cactactatt cactgatgca1320  
 gaaagacggt cttttgcata aaagactttt tttaacactt tggacttctc tgaaatattt1380  
 agaagtgtca atttctggcc ccccccaac aggaattcta tagtaagggg gaggagaagg1440  
 ggggctcctt cctctcctc gaatgacgtt atgggcacat gcctttttaa agttcttta1500  
 gcaacacaga gctgagtcct ctttgtcata cttttggatt tagtgtttca tcagctgttt1560  
 ttagtataaa acattttgtt aaaatagata ttggttttaa tgatacagta ttttaggtat1620  
 gatttaagac tatgatttac ctatacatta tatatatttt ataaagatac taaaccagca1680  
 tacccttact ctgccagagt agtgaagcta attaaacacg tttggtttct gaataaattg1740  
 aactaaatcc aaactatttc ctaaaatcac aggacattaa ggaccaatag catctgtgcc1800  
 agagatgtac tgttatttag tgggaagacc aattctaaca gcaaataaca gtctgagact1860  
 cctcatacct cagtggtag aagcatgtct ctcttgagct acagtagagg ggaagggatt1920  
 gttgtgtagt caagtcacca tgctgaatgt acactgattc ctttatgatg actgcttaac1980  
 tccccactgc ctgtcccaga gaggttttcc aatgtagctc agtaattcct gttactttac2040  
 agacaggaaa gttccagaaa ctttaagaac aaactctgaa agacctatga gcaaatgggtg2100  
 ctgaataactt tttttttaa gccacatttc attgtcttag tcaaagcagg attattaagt2160  
 gattatttaa aattcgtttt tttaaattag caacttcaag tataacaact ttgaaactgg2220  
 aataagtgtt tattttctat taataaaaat gaattgtgac aaaaaaaaaa aaaggcttcg2280  
 gcttttgaag tctatgtgtg ggggggggggt 2310

002221 0042250

## (2) INFORMATION ON SEQ ID NO. 3:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 854 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

ctgcacgggg gctcgggctc actataaaaag gtgggagcgc gtggtgcccc agcaacgacg 60
agtttcagaa cgatggagag ctcccgcgtg aggcctgctgc ccctcctggg cgccgccctg120
ctgctgatgc tacctctgtt gggtagccgt gccagggagg acgccgagct ccagccccga180
gccctggaca tctactctgc cgtggatgat gctcccacg agaaggagct gatcgaagcg240
ctgcaagaag tcttgaagaa gctcaagagt aaacgtgttc ccattctatga gaagaagtat300

ggccaagtcc ccattgtgtga cgccggtgag cagtgtgcag tgaggaaagg ggcaaggatc360
gggaagctgt gtgactgtcc ccgaggaaac tcctgcaatt ccttcctcct gaagtgetta420
tgaaagggcg tccattctcc tccatacatc cccatccctc tactttcccc agaggaccac480
accttcctcc ctggagtttg gcttaagcaa cagataaaagt ttttattttc ctctgaaggg540
aaagggtctt tttcctgctg tttcaaaaat aaaagaacac attagatgtt actgtgtgaa600
gaataatgcc ttgtatggtg ttgatacgtg tgtgaagtat tcttatttta tttgtctgac660
aaactcttgt gtacctttgt gtaaagaagg gaagctttgt ttgaaaattg tattttttgta720
tgtggcatgg cagaatgaaa attagatcta gctaattctg gtagatgtca ttacaacctg780
gaaaataaat caccctaagt gacacaaatt gaagcatgta caaattatac ataataaagt840
gtttttaata attg                                     854

```

## (2) INFORMATION ON SEQ ID NO. 4:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

002221 004E2950

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

cgccagcccc gtcggggggcc cggagggggac tcggagcggg ccaagggggcg gctccggcgg 60
gcggactcgg agcggggcggc ggagtgaacc ggacagctgt cctctctgac accaccccg 120
cctgcctctt tgttgccatg agagctgcct acctcttctt gctattcctg cctgcaggct 180
tgctggctca gggccagtat gacctggacc cgtctcggcc gttccctgac cacgtccagt 240
acaccacta tagcgaccag atcgacaacc cagactacta tgattatcaa gaggtgactc 300
ctcggccctc cgagggaacag ttccagttcc agtcccagca gcaagtccaa caggaagtca 360
tcccagcccc aaccccagaa ccaggaaatg cagagctgga gccacagag cctgggcctc 420
ttgactgccg tgagggaacag taccctgca cccgcctcta ctccatacac aggccttgca 480
aacagtgtct caacgaggtc tgcttctaca gcctccggcg tgtgtacgtc attaacaagg 540
agatctgtgt tcgtacagtg tgtgcccatt aggagctcct ccgagctgac ctctgtcggg 600
acaagtcttc caaatgtggc gtgatggcca gcagcggcct gtgccaatcc gtggcggcct 660
cctgtgccag gagctgtggg agctgctagg gtgggtgctgg catcctgagt cctggccctc 720
ctgggatctg gggccctcgg gccctgcctg acctgggtgt tttttccca tcccctggt 780
ccttttatte tgtaaaaagt tagtggaact cagccctggg ggttgcaagg tcggtgcct 840
caggcccttc cttcagcctg tggccacctc tggggcagca tgggggctcc ccactgcca 900
gtctgccctc cgggttgggg gagtatccca ggccctctct tgggaccctg ggccctgacg 960
ggccttctca gcccggtttt aggacagaca gtcccccgag gtaggctaca tccccccacc 1020
ccagctgggtc tgcttggtt tctacagcc ccgtgggca tggaccacct ttattttata 1080
caaaattaaa aacaagtttt tacaaaaaaa aa 1112

```

## (2) INFORMATION ON SEQ ID NO. 5:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1051 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

00673400.12300

## (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

gcgcaggcgc gaagaagctg gcaggggcac gagccggggg cgggtttgaa gacgcgtcgt 60
tgggttttgg aggccgtgaa acagccgttt gagtttggct gcgggtggag aacgtttgtc 120
aggggccccg ccaagaagga ggcccgccgt ttacgatggt gtccatgagt ttcaagcgga 180
accgcagtga ccggttctac agcaccgggt gctgcggctg ttgccatgtc cgcaccggga 240
cgatcatcct ggggacctgg tacatggtag taaacctatt gatggcaatt ttgctgactg 300
tggaagtgac tcatccaaac tccatgccag ctgtcaacat tcagtatgaa gtcacggta 360
attactattc gtctgagaga atggctgata atgcctgtgt tctttttgcc gtctctgttc 420
ttatgtttat aatcagttca atgctggttt atggagcaat ttcttatcaa gtgggttggc 480
tgattccatt ctctgtttac cgactttttg acttcgtcct cagttgcctg gttgctatta 540
gttctctcac ctatttgcca agaatacaag aatatctgga tcaactacct gatttccct 600
acaaagatga cctcctggcc ttggactcca gctgcctcct gttcattgtt cttgtgttct 660
ttgccttatt catcattttt aaggcttatt taattaactg tgtttggaac tgctataaat 720
acatcaacaa ccgaaacgtg ccggagattg ctgtgtaccc tgcctttgaa gcacctctc 780
agtacgtttt gccaacctat gaaatggccg tgaaaatgcc tgaaaaagaa ccaccacctc 840
cttacttacc tgctgaaga aattctgcct ttgacaataa atcctatacc agctttttgt 900
ttgtttatgt tacagaatgc tgcaattcag ggctcttcaa acttgcttag atataaaata 960
tggtggccct ttggttttaa agcaatttat ttccaaaac actaaggag cctttttgga 1020
catctggtta aacggccttt ttgggttttt t

```

## (2) INFORMATION ON SEQ ID NO. 6:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1516 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002221-001E2950

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

gttgctctca tccctctcat acaggggtgac caggacgttc ttgagccagt cccgcatgcg 60
cagggggaag aagatccatg agaaggagaa gcgcctggag gcaggagacc accccgtgga 120
gctgctggcc cgggacttcg agaagaacta taacatgtac atcttccctg tacactggca 180
gttcggccag ctggaccagc accccattga cgggtacctc tcccacaccg agctggctcc 240
actgctgct cccctcatcc ccattggagca ttgcaccacc cgctttttcg agacctgtga 300
cctggacaat gacaagtaca tcgccctgga tgagtgggcc ggctgcttcg gcatcaagca 360
gaaggatata gacaaggata ttgtgatcta aatccactcc tcccacagta cgggattctc 420
tctttaaccc tcccttcgtg gtttcccca atgtttaaaa tgtttggatg gtttgtgtt 480
ctgcctggag acaagggtgct aacatagatt taagtgaata cattaacggt gctaaaaatg 540
aaaattctaa cccaagaaca tgacattctt agctgtaact taactattaa ggccttttcc 600
acacgcatta atagtcccat ttttctcttg ccattttagt ctttgcccat tgtcttattg 660
ggcacatggg gtggacacgg atctgctggg ctctgcctta aacacacatt gcagcttcaa 720
cttttctctt tagtgttctg tttgaaacta atacttaccg agtcagactt tgtgttcatt 780
tcatttcagg gtcttggtcg cctgtgggct tccccagggt gcctggaggt gggcaaaagg 840
aagtaacaga cacacgatgt tgtcaaggat ggttttggga cttagaggctc agtgggtggg 900
gagatccctg cagaacccac caaccagaac gtggtttgcc tgaggctgta actgagagaa 960
agattctggg gctgtgttat gaaaatata acattctcac ataagcccag ttcataacca 1020
tttctctctt tacctttcag tgcagtttct tttcacatta ggctgttggt tcaaactttt 1080
gggagcacgg actgtcagtt ctctgggaag tggtcagcgc atctgcagg gcttctctct 1140
ctctgtcttt tggagaacca gggctcttct caggggctct agggactgcc aggctgttct 1200
agccaggaag gccaaaatca agagtgaagt gtagaaagt gtaaaataga aaaagtggag 1260
ttggtgaatc ggttggtctt tcttcacatt tggatgattg tcataagggt tttagcatgt 1320
tctctctttt ctccaccctc cctttttttt ccccaagaat acagagaaaa ctcaaagttal 1380
atggggaggg tcggatccta caggcctgag aatcggtcaa ctccaagcat ttcattggaa 1440
aggcggttc ctaattaatc ctacaaacc ccaccaggga tggtagaggg tttcaccaat 1500
tcttcaaaaa ataaaa

```

## (2) INFORMATION ON SEQ ID NO. 7:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2367 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

007221-004E2950

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

cgccgggact cttggcgggg gaaggtgtgt gtcagctttt gcgtcactcg agccctgggc 60
gctgcttgct aaagagccga gcacgcgggt ctgtcatcat gtcgcgttac gggcggtacg 120
gaggagaaac caaggtgtat gttggtaacc tgggaactgg cgctggcaaa ggagagttag 180
aaagggcttt cagttattat ggtcccttaa gaactgtatg gattgcgaga aatcctccag 240
gatttgcttt tgtggaattc gaagatccta gagatgcaga agatgcagta cgaggactgg 300
atggaaaagg gattttgtgg tcccagtgga gggttgaact atcgacaggc atgcctcgga 360
gatcacgttt tgatagacca cctgcccagc gtccctttga tccaaatgat agatgctatg 420
agtgtggcga aaagggacat tatgcttatg attgtcatcg ttacagccgg cgaagaagaa 480
gcaggtcacg gtctagatca cattctcgat ccagagggaag gcgatactct cgctcacgca 540
gcaggagcag gggacgaagg tcaaggtcag catctcctcg acgatcaaga tctatctctc 600
tcgtagatc aagatcagct tcaactcaga gatctaggtc tggttctata aaaggatcga 660
ggtatttcca atccccgtcg aggtcaagat caagatccag gtctatttca cgaccaagaa 720
gcagccgac aaagtccaga tctccatctc caaaaagaag tcgttcccca tcagggaagtc 780
ctcgcagaag tgcaagtcct gaaagaatgg actgaagctc tcaagttcac cctttaggga 840
aaagttattt tgtttacatt attataaggg atttgtgatg tctgtaaagt gtaacctagg 900
aaagataatt caacctctta atcaaaatgg atctggatta ctatgtaaat tcacagcagt 960
aagataatat aaattttgtt gaatgtatta acatcatatg gtctgaaaaat gtgggttttt 1020
atttggcaca tttaaataaa atgtttctaa ctgatttttt gatttgtgtt caatattaac 1080
acttcttaat ttgatatatt tgagagtcag acattataat tgttaacctt attcatacat 1140
acctacattc agaattgaaa ggtgttgggt aagtcttgaa catcactatt ctatgcataa 1200
aacttggcca ggatcttaag ggactttgaa aattccatct tacccttgta gctctgggt 1260
agatgacctg agtcccttat gatacagcct gaatgcatca tgacagatcc ttaagttagc 1320
taatccgttt gaagttgggt ttagtaggta ttgtatgatc agtgggtgaag caagtaggac 1380
cactgatgtg tctaaatgag catgacagga actaaacgaa actgattaaa tgtatgagaa 1440
atagaaaactg atttctggat gatctttata ctaattgcag ctttcaggct actaggtggc 1500
atagtgttaa ttaggactcc ccaagatatg gggagtctta ctctcaatgg tcttgtttct 1560
ttgctttcta cattagttaa ccagttttat accaaaaaat gcatgtttga ggaattgtct 1620
gaaattggga caaaacacct tcatgtaaac cagctttgca aaattttcca gccagatac 1680
tcttcattct tccaatgga ttgtcttatt ctgagcaaaag acctgttgtt aatcttcaag 1740
ctaggttttg cagttcccaa ccacaacatt ctctattttt gccaggctgg tgcaaaagta 1800
ttaaagatgt caatcagaaa tgtcaatgag actaaagtgg ttttgtaaat ctacgtata 1860
tttagcaaca ctccatgtag ctaatatttt ttggtagcat ctggtagacc ttagaatgtt 1920
acatagccag taggttcttt attcaaattt taagtatctt aagaatagta gggcagtaac 1980
agttactttt gagagttttc tggccaagct tttaccaggc attctctagc cttggtacaa 2040
aaaaaaaaaa aacctgctgg ttgcgcagat acctaggctt gtccatttta tgcatttcag 2100
caaagtcatt ggatactatt gcaacttggg aatactggtc tgcatcaagt ttattcggt 2160
gtttgaccgc tagtatgttg gaagttattt ggattgtttt tgggaattttg actggctgaa 2220
ttatggttgg tataaagtta tgtgtataac tggcaggctt atttatctgt tgcacttgg 2280
tagctttaat tgttctgtat tatttaaaga taagtttact caacaataaa tctgcagaga 2340
ttgaacaaat aaaaaaaaaa aaaaaaa

```

2367

002221 004E2960

## (2) INFORMATION ON SEQ ID NO. 8:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 568 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

ctcgagccgc  gggcagtggc  cgcgaatgcg  cggagacact  gaccttcagc  gcctcggctc  60
cagcgccatg  gcgccctcca  ggaagtctct  cgttggggga  aactggaaga  tgaacgggcg  120
gaagcagagt  ctgggggagc  tcctcggcac  tctgaacgcg  gccaaagggt  cggccgacac  180
cgaggtggtt  tgtgctcccc  ctactgccta  tatcgacttc  gcccggcaga  agctagatcc  240
caagattgct  gtggctgcgc  agaactgcta  caaagtgact  aatggggctt  ttactgggga  300
gatcagccct  ggcattgatc  aagactgcgg  agccacgtgg  gtggtcctgg  ggcactcaga  360
gagaaggcat  gtctttgggg  agtcagatga  gctgattggg  cagaaagtgg  cccatgctct  420
ggcagagggg  ctcggaagta  tcgctgcata  tggggagaag  ctagatgaaa  gggaaagctg  480
catcactgag  aatgttggtt  tcgagcagac  aaaggccatc  ggggatgact  tgaaggactg  540
gatcaagttc  gtccctggcc  gttggcct

```

## (2) INFORMATION ON SEQ ID NO. 9:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1775 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

09573400.123700

## (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ctcggggggcc attttgtgaa gagacgaaga ctgagcgggt gtggccgcgt tgccgacctc 60  
cagcagcagt cggcttctct acgcagaacc cgggagtagg agactcagaa tcgaatctct 120  
tctccctccc cttcttgtga gatttttttg atcttcagct acattttcgg ctttgtgaga 180  
aacctttacca tcaaacacga tggccagcaa cgttaccac aagacagatc ctgcctccat 240  
gaactcccgt gtattcattg ggaatctcaa cactcttggt gtcaagaaat ctgatgtgga 300  
ggcaatcttt tcgaagtatg gcaaaattgt ggctgctct gttcataagg gctttgcctt 360  
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gattgctggc cagggttttag atattaacct ggctgcagag ccaaaaagtga accgaggaaa 480  
agcaggtgtg aaacgatctg cagcggagat gtacggctcc tcttttgact tggactatga 540  
ctttcaacgg gactattatg ataggatgta cagttaccca gcacgtgtac ctccctctcc 600  
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aagggggcaa agtggccttc attctaagag tggacagcgg ggatcttcca agtctggaaa 720  
gttgaaagga gatgacctc aggccattaa gaaggagctg acccagataa aacaaaaagt 780  
ggattctctc ctggaaaaacc tggaaaaaat tgaaaaaggaa cagagcaaac aagcagtaga 840  
gatgaagaat gataagtcag aagaggagca gagcagcagc tccgtgaaga aagatgagac 900  
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aaaagaggct gaggaaggag aggatgacag agacagcgcc aatggcgagg atgactctta 1080  
agcacatagt ggggtttaga aatcttatcc cattatttct ttacctaggc gcttgcctaa 1140  
gatcaaattt ttcaccagat cctctccctc agtatcttca gcacatgctc actgttctcc 1200  
ccatccttgt ccttcccatg ttcattaat catattgcc cgcgctagt cccattttca 1260  
cttcccttga cgtcctagt agttttgtta agtcttacc tgtaattttt gcttttaatt 1320  
ttgatacctc tttatgactt aacaataaaa aggatgtagt gtttttatca actgtctcca 1380  
aaataatctc ttgttatgca gggagtacag ttcttttcat tcatacataa gttcagtagt 1440  
tgcttcccta actgcaaagg caatctcatt tagttgagta gctcttgaaa gcagcttga 1500  
gttagaagta tgtgtgttac accctcacat tagtgtgctg tgtggggcag ttcaacacaa 1560  
atgtaacaat gtatttttgt gaatgagagt tggcatgtca aatgcacct ctagaaaaat 1620  
aattagtgtt atagtcttaa gatttgttt ctaaaagtga tactgtgggt tattttgtg 1680  
aacagcctga tgtttgggac ctttttctc caaaataaac aagtccttat taaaccagga 1740  
atttggagaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1775

## (2) INFORMATION ON SEQ ID NO. 10:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 509 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:



(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

caggtcgagt ggccactgcg cagaccagac ttcgctcgta ctcgtgcgcc tcgcttcgct 60
tttcctccgc aaccatgtct gacaaaccgc atatggctga gatcgagaaa ttcgataagt120
cgaaactgaa gaagacagag acgcaagaga aaaatccact gccttcctaaa gaaacgattg180

aacaggagaa gcaagcaggg gaatcgtaat gaggcgtgcg ccgccaatat gcaactgtaca240
ttccacaagc attgccttct tattttactt cttttagctg ttttaactttg taagatgcaa300
agaggttgga tcaagtttaa atgactgtgc tgcccctttc acatcaaagg gactacttga360
acaacggaag ggccgcggcc tacctttccc atctgtctat ctatctggct ggcagggaag420
ggaagagttg caggttggtg aggaagaagt ggggtggaag aagttggatg ggccgccagt480
aaaacttggt taaaccgaac ttggccaag                               509

```

(2) INFORMATION ON SEQ ID NO. 11:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 2191 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

0042227 0042227 0042227

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

actgagcgag gccagccgt gccgcatcta caccgagcgc tgtggctccg gccttcgctg 60  
 ccagccgtcg cccgacgagg cgcgaccgct gcaggcgctg ctggacggcc gcgggctctg 120  
 cgtcaacgct agtgccgtca gccgcctgcg cgcctacctg ctgccagcgc cgcagctcc 180  
 aggaaatgct agtgagtcgg aggaagaccg cagcgccggc agtggtggaga gcccgctccg 240  
 ctccagcacg caccgggtgt ctgatcccaa gtccaacccc ctccattcaa agataatcat 300  
 catcaagaaa gggcatgcta aagacagcca gcgtacaaa gttgactacg agtctcagag 360  
 cacagatacc cagaacttct cctccgagtc caagcgggag acagaatatg gtccctgccg 420  
 tagagaaatg gaagacacac tgaatcacct gaagtccctc aatgtgctga gtcccagggg 480  
 tgtacacatt cccaactgtg acaagaaggg attttataag aaaaagcagt gtccgcccctt 540  
 caaaggcagg aagcggggct tctgctgggtg tgtggataag tatgggcagc ctctcccagg 600  
 ctacaccacc aaggggaagg aggacgtgca ctgctacagc atgcagagca agtagacgcc 660  
 tgccgcaagg ttaatgtgga gctcaaatat gccttatttt gcacaaaaga ctgccaagga 720  
 catgaccagc agctggctac agcctcgatt tatattttctg tttgtggtga actgattttt 780  
 tttaaaccaa agtttagaaa gaggtttttg aaatgcctat ggtttctttg aatggtaaac 840  
 ttgagcatct ttccactttc cagttagtcag caaagagcag tttgaatttt ctgtgcgtt 900  
 cctaccaaaa tattcagaga ctgagcaca gcaccagac ttcattgcgc cgtggaatgc 960  
 tcaccacatg ttggtcgaag cggccgacca ctgactttgt gacttaggcg gctgtgttgc 1020  
 ctatgtagag aacacgcttc acccccactc cccgtacagt gcgcacaggc tttatcgaga 1080  
 ataggaaaaac ctttaaacc cggtcattcc gagatcccaa cgcattgctc tggagctcac 1140  
 agccttctgt ggtgtcattt ctgaaacaag ggcgtggatc cctcaaccaa gaagaatgtt 1200  
 tatgtcttca agtgacctgt actgcttggg gactattgga gaaaataagg tggagtccta 1260  
 cttgtttaaa aaatatgtat ctaagaatgt tctagggcac tctgggaacc tataaaggca 1320  
 ggtatttctg gccctcctct tcaggaatct tcctgaagac atggcccagt cgaaggccca 1380  
 ggatggcttt tgcctgcggc ccggtgggta ggaggacag agagacaggg agagtcagcc 1440  
 tccacattca gaggcatcac aagtaatggc acaattcttc ggatgactgc agaaaatagt 1500  
 gttttgtagt tcaacaactc aagacgaagc ttatttctga ggataagctc tttaaaggca 1560  
  
 aagctttatt ttcattcttc atcttttgtc ctcccttagca caatgtaaaa aagaatagta 1620  
 atatcagaac aggaaggagg aatggcttgc tggggagccc atccaggaca ctgggagcac 1680  
 atagagattc acccatgttt gttgaactta gagtcattct catgcttttc tttataattc 1740  
 acacatatat gcagagaaga tatgttcttg ttaacattgt atacaacata gccccaaata 1800  
 tagtaagatc tatactagat aatcctagat gaaatgttag agatgctata tgatacaact 1860  
 gtggccatga ctgaggaaa gaggctcacc ccagagactg ggctgctctc ccggaggcca 1920  
 aacccaagaa ggtctggcaa agtcaggctc agggagactc tgccctgctg cagacctcgg 1980  
 tgtggacaca cgctgcatag agctctcctt gaaaacagag gggctcctca acattctgcc 2040  
 taccatttag cttttcttta tttttttaac tttttggggg gaaaagtatt tttgagaagt 2100  
 ttgtcttgca atgtatttat aaatagtaaa taaagttttt accattaaaa aaaaaaggag 2160  
 taaaaagaaa aaaaaggggc gccgccgact a 2191

09673400.122700

attatcttaca	tttcaaaata	attcccccta	atcgttttac	tcctaagttc	attaccattg	60
ttggcccacc	ttaggttcca	ccacttggtt	gttaccccag	ccctgggttc	aaacagggac	120
atggcaagg	gacacaggac	agaggggtcc	ccagctgcc	cctcaccac	cgcaattcat	180
ttagtagcag	gcacaggggc	agctccggca	cggctttctc	aggcctatgc	cggagcctcg	240
agggctggag	agcgggaaga	caggcagtg	tgggggagt	gcagcaggac	gtcaccagga	300
gggccaacg	ccacgggag	ggggccccgc	gacattgcgc	agcaaggagg	ctgcaggggc	360
tgggcctgc	ggcgccggtc	ccacgaggca	ctgcggccca	gggtctggtg	cggagagggc	420
ccacagtga	cttggtgacg	ctgtatgcc	taccgcgtca	ggcctgggg	ctggctggc	480
agacagtaca	gcattcaggg	gagtcaagg	catggggcga	gaccagacta	ggcgaggcgg	540
gcggggcgga	gtgaatgagc	tctcaggagg	gaggatggtg	caggcagggg	tgaggagcgc	600
agggggcggc	gagcgggag	cactggcctc	cagagccgt	ggccaaggcg	ggcctcgcg	660
gcggcgacg	agccgggatc	ggtgcctcag	cgttcgggct	ggagacgag	ccaggtctcc	720
agctggggtg	gacgtgccca	ccagctgcc	aaggcaagac	gccaggtccg	gtggacgtga	780
caagcaggac	atgacatggt	ccggtgtgac	ggcgaggaca	gaggaggcgc	ctccggcctt	840
cctgaacac	ttaggctggt	gggctgcgg	caagaagcgg	gtctgtttct	ttactctctc	900
cacggagtc	gcacactatg	gctgccctct	gggtctccag	aaccacaac	atgaaagaaa	960
tgtgtctacc	cagctcaagc	ctgggccttt	gaatccggac	acaaaaccct	ctagcttggal	1020
aattgaatatg	ctgcacttta	caaccactgc	actacctgac	tcaggaatcg	gctctggaag	1080
gtgaagctag	aggaaccaga	cctcatcagc	ccaacatcaa	agacaccatc	ggaacagcag	1140
cgcgccgagc	accacccccg	caccggcgac	tccatcttca	tggccacccc	ctgcggcgga	1200
cggttgacca	ccagccacca	catcatccca	gagctgagct	cctccagcgg	gatgacgccg	1260
tccccaccac	ctccctcttc	ttctttttca	tcctttctgtc	tctttgtttc	tgagctttcc	1320
tgtctttcct	tttttctgag	agattcaaa	cctccacgac	tctgtttccc	ccgtcccttc	1380
tgaatttaat	tgcactaag	tcat ttgcac	tggttggagt	tgtggagacg	gccttgagtc	1440
tcagtacgag	tgtgcgtgag	tgtgagccac	cttggcaagt	gcctgtgcag	ggcccgcccg	1500
ccctccatct	gggcgggggtg	actgggcgcc	ggctgtgtgc	ccgaggcctc	accctgcctt	1560
cgcctagtct	ggaagctccg	accgacatca	cggagcagcc	ttcaagcatt	ccattacgcc	1620
ccatctcgct	ctgtgccttc	ccccaccagg	gcttcagcag	gagccctgga	ctcatcatca	1680
ataaacactg	ttacagcaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1740
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa				1769

## (2) INFORMATION ON SEQ ID NO. 13:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

aaaagctgtc cgcgcgggga gccagggcc agctttgggg ttgtccctgg acctgtcttg 60
gttccagaac ctgacgaccc ggcgacggcg acgtctcttt tgactaaaag acagtgtcca 120
gtgctccagc ctaggagtct acggggaccg cctcccgcgc cgccaccatg cccaacttct 180
ctggcaactg gaaaatcatc cgatcggaaa acttcgagga attgctcaaa gtgctggggg 240
tgaatgtgat gctgaggaag attgctgtgg ctgcagcgtc caagccagca gtggagatca 300
aacaggaggg agacactttc tacatcaaaa cctccaccac cgtgcgcacc acagagatta 360
acttcaagggt tggggaggag tttgaggagc agactgtgga tgggaggccc tgtaagagcc 420
tggtgaaatg ggagagttag aataaaatgg tctgtgagca gaagctcctg aaggagagg 480
gccccaaagc ctctgtggacc agagaactga ccaacgatgg ggaactgatc ctgaccatga 540
cggcggatga cgttgtgtgc accagggtct acgtccgaga gtgagtggcc acaggtagaa 600
ccgcggccga agcccaccac tggccatgct caccgccctg cttcactgcc cctccgtcc 660
caccctctcc ttctaggata gcgtccctc taccocagtc acttctgggg gtcactggga 720
tgctctttgc agggctcttg tttctttgac ctctctcttc ctccctaca ccaacaaaga 780
ggaatggctg caagagccca gatcacccat tccgggttca ctcccgcct cccaagtca 840
gcagtcctag ccccaaacca gccagagca ggggtctctt aaaggggact tgagggcctg 900
agcaggaaa actggccctc tagcttctac cctttgtccc ttagcctat acagtttaga 960
atatattttt gttattttta ttaaaatgct ttaaaaaaat aaaaaaaaaa aaaaaaaaaa 1020
aaaaaa                                     1026

```

## (2) INFORMATION ON SEQ ID NO. 14:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 676 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

002221 004E2950

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

ggccatttttg tgaagagacg aagactgagc ggttggtggcc gcgttgccga cctccagcag 60
cagtcgggctt ctctacgcag aaccggggag taggagactc agaatcgaat ctcttctccc120
tccccttctt gggcagcaag gcgaaccca tccctactca ctggagctca gctttgattt180
ttaacctccc tccccacccc ttccagaaca cacacattcc attccaaaac tgattttata240
aagacatttt aaacataatg atgcaacttg gtgtgcacta cagcaaatgt acagggtgtt300
tttttttaat tgtttccaaa accgggacct ggatttaaga tgtaattttt aaaattttcta360
tttctatttt ttccggcagca gttgggttag aggaggagga gccttttagc ctcccagaaa420
ctgacctctc tacttctctg tgtattttta agattgattg atgatgtgga aagggccttg480
cttgtctgct actgaaaact ttatccttgc ggtttttgtg gaactgcgtt tggaaagaga540
aaagaaatga actttactga cttgacattt tgcacctccc ggttttcgaa tctgggcaat600
tttaattttg gttttacagt gagagttttt gatctcagca cagaagtaat ccaatttttt660
ttagcatttt ccgact
676

```

(2) INFORMATION ON SEQ ID NO. 15:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1254 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

004227.004227.00

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

cggtctgagc agctcgagcg gctcaaacac ctcatTTgac cttgccagct gaccttcaaa 60
ccctgcattt gaaccgacca acattaaGtc cagagagtaa acttgaatgg aataacgaca 120
ttccagaagt taatcatttg aattctgaac actggagaaa aaccgaaaaa tggacggggc 180
atgaagagac taatcatctg gaaaccgatt tcagtggcga tggcatgaca gagctagagc 240
tcgggcccag ccccgaggctg cagcccattc gcaggcaccc gaaagaactt ccccgatag 300
gtggtccttg aaaggacatt tttgaagatc aactatatct tcctgtgcat tccgatggaa 360
tttcagttca tcagatgttc accatggcca ccgcagaaca ccgaagtaat tccagcatag 420
cggggaagat gttgaccaag gtggagaaga atcacgaaaa ggagaagtca cagcacctag 480
aaggcagcgc ctctcttcca ctctcctctg attagatgaa actgttacct taccctaaac 540
acagtatttc tttttaactt ttttatttgc aaactaataa aggtaatcac agccaccaac 600
attccaagct accctgggta cctttgtgca gtagaagcta gtgagcatgt gagcaagcgg 660
tgtgcacacg gagactcatc gttataattt actatctgcc aagagttaga agaaaggctg 720
gggatatttg ggttggcttg gttttgattt tttgcttggt tgtttgtttt gtactaaaac 780
agtattatct tttgaatatc gtaggacatc aagtatatac atgttatcca atcaagatgg 840
ctagaatggt gcctttctga gtgtctaaaa cttgacaccc ctggtaaatc tttcaacaca 900
cttccactgc ctgcgtaatg aagttttgat tcatttttaa ccactggaat ttttcaatgc 960
cgtcattttc agttagatga ttttgcaatt tgagactaaa atgccatgtc tatttgattal1020
gtcttatttt tttattttta caggcttatt agtctcactg ttggctgtca ttgtgacaaa1080
gtcaataaaa cccccaagga cgacacacag tatggatcac atattgtttg acattaagct1140
tttgccagaa aatgttgcat gtgttttacc tcgacttgct aaaatcgatt agcagaaagg1200
catggctaata aatgttggtg gtgaaaataa ataaataagt aaacaaaaag aaaa 1254

```

## (2) INFORMATION ON SEQ ID NO. 16:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 537 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673400-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

ggccccggggcc cccaccctcg acatgcgctt ccggcgacgc cttagcgctg acccccacgc 60
aaccacagcga aactccgcgg aggcgcgcgg cacgatggac ggtcgggtgc agctgatgaal20
ggccctcctg gccggggccc tccggcccgc ggcgcgctgc tggaggaacc cgattccctt180
tcccagagacg tttagcggag ataccgaccg actcccgag ttcatcgtgc agacgtgctc240
ctacatgttc gtggacgaga acacgtttct caacgacgcc ctgaagggtga cgttcctcat300
caccgcctc acggggccag ccctgcagtg ggtgatcccc tacatcagga aggagagccc360
cctgctcaat gattaccggg gctttctggc cgagatgaag cgagctttg gatgggagga420
ggacgaggac ttctaggccg ggagaccctc gggcctgggg gcgggtgctc tgggaagagt480
tcgctgtgcc agtgccacc gctagggtct ccacaggcgc cctccccagg gaatgct 537

```

## (2) INFORMATION ON SEQ ID NO. 17:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 823 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

tagactgaac aggaggggga gtcctgggta gcgcgcgggt ctaaateggt acttggcgga 60
aagttcccat gagtctttgc cagcgtcccc ctctttttgt gaggattggg atattccgac120
tccttaaggc cctgggcgac ataagggtgt accttttcat tcccgttgtt atggagggcc180
acatctgcca gagcctggag tctgcgaagg ccgggacccg gttccccggc ccacagtggg240
ggtgtgcaaa cccgagagaa ctgggttgca aattcgtgaa gaatcagcat catgtttggc300
agctgagtat tggagccagg agcctgccat gaggttttga gaacagagt ctgttttaga360
gctggcagca gcattctcagc ccaagagaag gttatatcc cagaggatgt cagtcccaag420
gaccagtagc tgccatcagt ttggattctg aaaactaact ggcattcaaca ctgggtgtag480
aaacatgctt gccttatgta tcagaggaca tgctcagcag atccaagaga tatatttggc540
aaacttttct agaaaaggca cattgggtat cattcattac attcttgagg tttttttggg600
tttttttttt ttttttttga gacagtcttg ctgtattgcc caggctggga gtgtggtggc660
acaatcacag ctcatgcat cctcaatcac ccagggccta agcaatcctc ccaccttgta720
gctgggacta cagctcacag cacaccgggc taaaattttt ttttgttgag acgggtttttc780
tatgttgccc ggggtggtttt cagggtccgg ggttcagatg gtc 823

```

00673400 123700

## (2) INFORMATION ON SEQ ID NO. 18:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

gggcgcacat aaggtgtgac cttttcattc ccgttggtat ggagggccac atctgccaga 60
gcctggagtc tgcgaaggcc gggacccggt tccccggccc acagtggggg tgtgcaaacc 120
cgagagaact ggtcgctgaa acctctacaa cttagttgac cgtaactgcc agagccctgc 180
cctgaattcc tgtccttact ccctctttaa gattgcgtac ccactgcaga gtgctgaaga 240
cggggtagcc acgaggttgc aaattcgtga agaatcagca tcatgtttgg cagctgagta 300
ttggagccag gagcctgcca tgagggtttg agaacagagt gctgttttag agctggcagc 360
agcatctcag cccaagagaa ggttatattc ccagaggatg tcagtcccaa ggaccagtag 420
ctgccatcag tttggattct gaaaactaac tggcatcaac actgggtgta gaaacatgct 480
tgccttatgt atcagaggac atgctcagca gatccaagag atatatattg caactttttc 540
tagaaaaggc acattgggta tcattcatta cattcttgag tttttttggg tttttttttt 600
ttttttttga gacagtcttg ctgtattgcc caggctggag tgtggtggca caatcacagc 660
tcattgcac ctaatcaccc caggcctaag caatcctccc accttgtagc tgggactaca 720
gctcacagca cacctggcta aaattttttt tttgttgaga cggattctct atgttgccca 780
ggctgggtctc aggtcctctg gctcagatgg tctcctgcc tcagcttcca aaggcacagg 840
ccaagttgta gctttgtccc ttgccatcat gcccaacaag aggttctata ccttttaattg 900
aattgacttt cataaattgg ttatgttggg gggcaagttc tttaagctgg aaattgtaaa 960
ttcctcctga aatgtttttt catgcagtta ccatgaacta atactacaat aaaggatggt 1020
cttgggtgtc aaaaaaaaaa aaaaaaaaaa aaaaagaaaa aaaaaaaaaa aaaaaaaaaa 1080
aa
1082

```

## (2) INFORMATION ON SEQ ID NO. 19:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

002221-004E2950



(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

cccattccat agggaatgag ctgggctgtc ctttctcccc acgttcacct gcacttcggt 60
agagagcagt gttcacatgc cacaccacaa gatccccaca atgacataac tccattcaga 120
gactggcgtg actgggctgg gtctccccac ccccccttc agctcttgta tcaactcagaa 180
tctggcagcc agttccgctc tgacagagtt cacagcatat attggtggat tcttgtccat 240
agtgcctctg ctttaagaat taacgaaagc agtgtcaaga cagtaaggat tcaaacatt 300
tgccaaaaat gagtctaagt gcatttactc tcttcctggc attgattggt ggtaccagt 360
gccagtacta tgattatgat tttccctat caatttatgg gcaatcatca ccaaactgtg 420
caccagaatg taactgccct gaaagctacc caagtgccat gtactgtgat gagctgaaat 480
tgaaaagtgt accaatggtg cctcctggaa tcaagtatct ttaccttagg aataaccaga 540
ttgaccatat tgatgaaaag gcctttgaga atgtaactga tctgcagtggt ctcatcttag 600
atcacaaact tctagaaaac tccaagataa aaggggagagt tttctctaaa ttgaaacaac 660
tgaagaagct gcatataaac cacaacaacc tgacagagtc tgtgggcca cttcccaaat 720
ctctggagga tctgcagctt actcataaca agatcacaaa gctgggctct tttgaaggat 780
tggtaaacct gaccttcact catctccagc acaatcggct gaaagaggat gctgtttcag 840
ctgcttttaa aggtctttaa tcaactgaa accttgactt gagcttcaat cagatagcca 900
gactgccttc tggctctcct gtctctcttc taactctcta cttagacaac aataagatca 960
gcaacatccc tgatgagtat ttcaagcgtt ttaatgcatt gcagtatctg cgtttatctc 1020
acaacgaact ggctgatagt ggaatacctg gaaattcttt caatgrgtca tccctggttg 1080
agctggatct gtccataaac aagcttaaaa acataccaac tgtcaatgaa aaccttgaaa 1140
actattacct ggaggtcaat caacttgaga agtttgacat aaagagcttc tgcaagatcc 1200
tggggccatt atcctactcc aagatcaagc atttgcgttt ggatggcaat cgcctctcag 1260
aaaccagtct tccaccggat atgtatgaat gtctacgtgt tgctaacgaa gtcactctta 1320
attaatatct gtatcctgga acaatatatt atggttatgt tttctgtgtg gtcagttttc 1380
atagtatcca tattttatta ctgtttatta cttccatgaa ttttaaaatc tgagggaaat 1440
gttttctaaa cattttattt tttttaaagg aaaaggatgg aaaggccagg gcctaatttc 1500
catccaccaa ggaacacacc acattattcc acggaatagg ccatcggg
1548

```

(2) INFORMATION ON SEQ ID NO. 20:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 844 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

09573400.12200

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```
acctgcagag ggggtccatac ggcgttggtc tggattcccg tcgtaactta aagggaaatt 60
ttcacaaatgt ccggagccct tgatgtcctg caaatgaagg aggaggatgt ccttaagttc120
cttgcagcag gaacccactt aggtggcacc aatcttgact tccagatgga acagtacatc180
tataaaaagga aaagtgatgg catctatatc ataaatctca agaggacctg ggagaagctt240
ctgctggcag ctogtgcaat tgttgccatt gaaaaccctg ctgatgtcag tgttatatcc300
tccaggaata ctggccagag ggctgtgctg aagtttgctg ctgccactgg agccactcca360
attgctggcc gcttcaactc tggaaacctc actaaccaga tccaggcagc cttccgggag420
ccacggcttc ttgtggttac tgacccaggg gctgaccacc agcctctcac ggaggcatct480
tatgttaacc tacctaccat tgcgctgtgt aacacagatt ctctctgctg ctatgtggac540
attgcaatcc catgcaacaa caaggtaatg attttaggat ctagagtttg tgaatgcgtg600
ctctagaaaa aacattcctg tgcacattgt tagagcttgg agttgaggct actgactggc660
cgatgaactc gcaagtgtag gtatgtgtgt acatgagggg caagttttcg ctaacaccac720
aagggtctct ggcccaatga gtggagtgtg atagtaattc ttgctacaag tataacatta780
ctgcatgaca gctttgtgga gaaatgaaaa catttgaaa atagtgtgtt ctctgccttg840
tcca
```

844

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 862 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

002227 004E2950

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

gagcaagaga gaaggaggcc cagacagtga gggcaggagg gagagaagag acgcagaagg 60  
 agagcgagcg agagagaaaag ggttctggat tgggggggag agcaaggag ggaggaaggc120  
 ggtgagagag gcggggggcct cgggagggtg aaagggggga ggagaagggc ggggcacgga180  
 ggcccagagc agggacaaga ctccgactcc agctctgact tttttcgcg ctctcggtt240  
 ccaactgcagc catgtcactc ctcttgctgg tgggtctcagc ccttcacatc ctcatcttta300  
 tactgctttt cgtggccact ttggacaagt cctgggtggac tctccctggg aaagagtccc360  
 tgaatctctg gtacgactgc acgtggaaca acgacaccaa aacatgggccc tgcagtaatg420  
 tcagcgagaa tggctggctg aaggcggtgc aggtcctcat ggtgctctcc ctcatctct480  
 gctgtctctc ctcatcctg ttcattgttc agctctacac catgcgacga ggaggtctct540  
 tctatgccac cggcctctgc cagctttgca ccagcgtggc ggtgtttact ggcgcccttga600  
  
 tctatgccat tcacgcccag gagatcctgg agaagcacc cgcagggggc agcttcggat660  
 actgcttcgc cctggcctgg gtggccttcc ccttcgccc ggtcagcggc atcatctaca720  
 tccacctacg gaagcgggag tgagcgccc gctcgcctg gctgccccg ccccttccc780  
 gccccctcg ccgcgcgtcc tccaaaaaat aaaaccttaa ccgcggggaa aaaaaaaaaa840  
 aaaaagggaag gaaaaaaaaa aa 862

## (2) INFORMATION ON SEQ ID NO. 22:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 546 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

cccagccaag ggtccttcag gtaggaggtc ctgggtgact ttggaagtcc gtagtgtctc 60  
 attgcagata attttttagct tagggcctgg tggctaggtc ggttctctcc tttccagtcg120  
 gagacctctg ccgcaaaccat gctccgccag atcatcggtc aggccaaaga gcatccgagc180  
 ttgatccccc tctttgtatt tattggaact ggagctactg gagcaacact gtatctcttg240  
 cgtctggcat tgttcaatcc agatgtttgt tgggacagaa ataaccaga gccctggaac300  
 aaactgggtc ccaatgatca atacaagttc tactcagtga atgtggatta cagcaagctg360  
 aagaagggaac gtccagattt ctaaatgaaa tgtttcacta taacgctgct ttagaatgaa420  
 ggtcttccag aagccacatc cgcacaattt tccacttaac caggaaatat ttctcctctt480  
 aatgaatga aatcaatggt ggggggcgct attggaagcc ctattggggg tcaagtgttg540  
 aataaa 546

004222T 004E2960

## (2) INFORMATION ON SEQ ID NO. 23:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1591 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

gccgaggagc cgagcccgcc accccccgc cgcgccgcgc cgcgccatggg ctgcctcggg 60
aacagtaaga ccgaggacca gcgcaacgag gagaaggcgc aggtgaggcc aacaaaaaga 120
tcgagaagca gctgcagaag gacaagcagg tctaccgggc cagcaccgc ctgctgctgc 180
tgggtgctgg agaattctgtg aaaagcacca ttgtgaagca gatgaggatc ctgcatgtta 240
atgggtttaa tggagacagt gagaaggcaa ccaaagtgcg ggacatcaaa aacaacctga 300
aagaggcgat tgaaccatt gtggccgcca tgagcaacct ggtgcccccc gtggagctgg 360
ccaacccgga gaaccagttc agagtggact acattctgag tgtgatgaac gtgcctgact 420
ttgacttccc tcccgaattc tatgagcatg ccaaggctct gtgggaggat gaaggagtgc 480
gtgcctgcta cgaacgctcc aacgagtacc agctgattga ctgtgccag tacttcctgg 540
acaagatcga cgtgatcaag caggctgact atgtgccgag cgatcaggac ctgcttcgct 600
gccgtgtcct gacttctgga atctttgaga ccaagttcca ggtggacaaa gtcaacttcc 660
acatgtttga cgtgggtggc cagcgcgatg aacgcccga gtggatccag tgcttcaacg 720
atgtgactgc catcatcttc gtggtggcca gcagcagcta caacatggtc atccgggagg 780
acaaccagac caaccgcctg caggaggctc tgaacctctt caagagcatc tggacaaca 840
gatggctgag caccatctct gtgatcctgt tctcaacaa gcaagatctg ctgctgaga 900
aagtccttgc tgggaaatcg aagattgagg actactttcc agaatttgct cgctacacta 960
ctcctgagga tgctactccc gagcccgag aggaccacg cgtgaccgg gccaaagta 1020
tcattcgaga tgagtttctg aggatcagca ctgccagtgg agatggcggt cactactgct 1080
accctcattt cacctgcgct gtggacactg agaacatccg ccgtgtgttc aacgactgcc 1140
gtgacatcat tcagcgcag cacttctgtc agtacagct gctctaagaa gggaaaccccc 1200
aaatttaatt aaagccttaa gcacaattaa ttaaaagtga aacgtaattg tacaagcagt 1260
taatcaccca ccatagggca tgattaacaa agcaaccttt ccttcccccc gagtgaattt 1320
gcgaaacccc cttttccctt cagcttgctt agatgttcca aatttagaaa gcttaaggcg 1380
gcctacagaa aaaggaaaaa aggccacaaa agttccctct cactttcagt aaaaataaat 1440
aaaacagcag cagcaaacaa ataaaatgaa ataaaagaaa caaatgaaat aaatattgtg 1500
ttgtgcagca ttaaaaaaaaa tcaaaataaa aattaaatgt gagcaaaagg aaaaaaaaaa 1560
ggcaaaaggg gaaagaagaa aagggggggg g

```

1591

002221-004E2960

## (2) INFORMATION ON SEQ ID NO. 24:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 441 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

ggcaggcaga tacgttcgtc agcttgctcc tttctgcccg tggacgcccg cgaagaagca 60
tcgttaaagt ctctcttcac cctgccgtca tgtctaagtc agagtctcct aaagagcccg120
aacagctgag gaagctcttc attggagggt tgagctttga aacaactgat gagagcctga180
ggagccattt tgagcaatgg ggaacgctca cggactgtgt ggtaatgaga gatccaaaca240
ccaagcgctc caggggcttt ggggtttgtca catatgccac tgtggaggag gtggatgcag300
ctatgaatgc aaggccacac aagggtggatg gaagagttgt ggaaccaaag agagctgttt360
cagagaagat ttgaaaagcc aggtgccact tacctgtgaa aaggatatttg ttggtggatt420
aaggagcact tgagacatca c                                     441

```

## (2) INFORMATION ON SEQ ID NO. 25:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1131 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

004227 0042960

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

cgggaggtga aatccggttc taaccgggtcc ggggctccca gcgctataaa aactttataa 60  
 accccccgga gcccgcagcag tgtgaagaag aggcgagaac gacccccgga ccgaccaaag 120  
 cccgcgcgcc gctgcacccc gcgtccagca cctacgtccc gctgccgtcg ccgccgccac 180  
 catgcccag agaaaggctg aaggggatgc taaggagat aaagcaaagg tgaaggacga 240  
 accacagaga agatccgcga ggtgtctgc taaacctgct cctccaaagc cagagcccaa 300  
 gcctaaaaag gcccctgcaa agaagggaga gaaggtaccc aaagggaaaa agggaaaaagc 360  
 tgatgctggc aaggagggga ataaccctgc agaaaatgga gatgccaaaa cagaccaggc 420  
 acagaaagct gaaggtgctg gagatgccaa gtgaagtgtg tgcatttttg ataactgtgt 480  
 acttctggtg actgtacagt ttgaaatact attttttacc aagttttata aaaatgcaga 540  
 attttgtttt actttttttt tttttttaa agctatgttg ttagcacaca gaacacttca 600  
 ttgttgtttt tgggggaagg ggcataatgc actaatagaa tgtctccaaa gctggattga 660  
 tgtggagaaa acacctttcc cttctagttt tgagagactt cctcttggtt ccagaggaga 720  
  
 gggattccct gactttgaca cacatggcca ccttggcaca aaagccttgt ggtatagaaa 780  
 aacaaatttg tttttatgtc ctcttctccc ttccatctt tcagcataga cttaactccc 840  
 ttaagcccag acatctgttg agacctgacc cctagtcatt ggttaccagt gtgtcaggca 900  
 atctggactt tccagtgatg cactgagat ggcacctgtc aaaagagcag tggttccatt 960  
 tctagattgt ggatcttcag ataaattctg ccattttcat ttcacttcct gaaagtcagg1020  
 gtcggcttgt gaaaagtgtg taaacaacat gctaaatgtg aaatgtcaac cctcactcta1080  
 aaacttttcc ctgggtcaga ggatccgatg gaggacttca attgggggtt t 1131

## (2) INFORMATION ON SEQ ID NO. 26:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

09673400.132700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

gtaccctcaa agacagagac accaagaaga atcgggaacat acaggcctttg atatcaaagg 60
tttataaaagc caatatctgg gaaagagaaa accgtgagac ttccagatct tctctggtga 120
agtgttggtt cctgcaacga tcacgaacat gaacatcaaa ggatcgccat ggaaagggtc 180
cctcctgctg ctgctggtgt caaacctgct cctgtgccag agcgtggccc ccttgcccat 240
ctgtcccggc ggggctgccc gatgccaggt gacccttcga gacctgtttg accgcgccgt 300
cgctcctgtcc cactacatcc ataacctctc ctccagaaatg ttcagcgaat tcgataaacg 360
gtatacccat ggccgggggt tcattaccaa ggccatcaac agctgccaca cttcttccct 420
tgccaccccc gaagacaagg agcaagccca acagatgaat caaaaagact tcttgagcct 480
gatagtcagc atattgcgat cctggaatga gccctctgtat catctggtca cggaaagtacg 540
tggtatgcaa gaagccccgg aggcctatcct atccaaagct gtagagattg aggagcaaac 600
caaacggctt cttagagggca tggagctgat agtcagccag gttcatcctg aaaccaaaga 660
aaatgagatc taccctgtct ggtcgggact tccatccctg cagatggctg atgaagagtc 720
tcgcctttct gcttattata acctgctcca ctgcctacgc agggattcac ataaaatcga 780
caattatctc aagctcctga agtgccgaat catccacaac aacaactgct aagcccacat 840
ccatttcacg tattcttgag aaggctcctta atgatccgtt ccattgcaag cttcttttag 900
ttgtatctct tttgaatcca tgcttggtg taacaggtct cctcttaaaa aataaaaaact 960
gactccttag agacatcaaa atctaaaaaa acttaattggg ccgggcgcag tggctcatgg 1020
ctgtggtccc ggcactttgg gaggccgagg caggcggtac aggaggtcag g 1071

```

## (2) INFORMATION ON SEQ ID NO. 27:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 896 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673400.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

gtgaccgggt cagaccgggt ctggagacaa aaggggcccgc ggcggccgga ggcgggacggg 60
cccggcgcgg gagggagcga agagcgccgg cagcgagcga gatgcagcac cgaggcttccl20
tccctcctcac cctcctcgcc ctgctggcgc tcacctccgc ggtcgccaaa aagaaagata180
aggtgaagaa gggcgccccc gggagcgaat gcgctgagtg ggcttggggg cctgcacccc240
ccagcagcaa ggattgcggc gtgggtttcc gcgagggcac ctgcggggcc cagaccagc300
gcatccgggt caggggtccc tgcaactgga agaaggagt tggagccgac tgcaagtaca360
agtttgagaa ctgggtgctg tgtgatgggg gcacaggcac caaagtccgc caaggcacc420
tgaagaaggc gcgctacaat gctcagtgcc aggagaccat ccgctgcacc aagccctgca480
cccccaagac caaagcaaaq gccaaagcca agaaaggga gggaaaggac tagacgcaa540
gcctggatgc caaggagccc ctggtgtcac atggggcctg gccacgccc tccctctccc600
aggcccagag tgtgaccac cagtgccttc tgtctgctcg ttagctttaa tcaatcatgc660
cctgccttgt cctctcact cccagcccc accctaagt gcccaaagt gggagggaca720
agggattctg ggaagcttga gctccccc aagcaatgt agtcccagag ccgcttttg780
tcttcccca caattccatt actaagaaac acatcaaata aactgacttt tccccccaa840
aaaaagctct tcttttttaa tataaaaaaa aaaaaaaaaa aaaaaaaaaa aagaaa 896

```

## (2) INFORMATION ON SEQ ID NO. 28:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1050 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

ttttcatttt tttttttttt tttttctcag ttcaagttaa atacaaacta caaaagatta 60
atgggttgct ctactaatat atcatacaaa ccagtagcct gccacaacg ccaactcagg 120
ccattcctac caaaggaaga aaggctggct tctccacccc ctgtaggaaa ggcctgcctt 180
gtaagacacc acaattcggc tgaatctgaa gtcttggttt ttactaatgg aaaaaaaaaa 240
tacagaagag gttttgttct catggctgcc caccgcagcc tggcactaaa acagcccagc 300
gtcactttct gcttgagaaa atattctttg ctcttttgga catcaggctt gatggtatca 360
ctgccagggt tccagccagc tgggcacact tccccatgtt tgtcagttaa ctggaaggcc 420
tgaactagtc tcaaagtctc atccacagag cggccaacag ggaggtcatt tacagtgate 480
tgccgaagaa tacccttatc atcaatgata aaaaggcccc tgaacgagat gccttcatca 540
gcctttaaga ccccataatc ctgagcaatg gtgcgcttcg ggcttgatac caaaggaatg 600
ttcatgggtc ccagtcctcc ttgtttctta ggtgtattga cccatgctag atgacagaag 660
tgagaatcca cagaagcacc aatcacttgg cagttgagtt tcttaaattc ttctgcccta 720
tcaactgaaa caatgatctc cgtggggcac acaaagggtga agtcaagagg gtaaaagaag 780
aacacaacat attttccttt gtagtcagac aggctgatat ctttaaactg accatctggc 840
ataacagctg tggctttgaa gttgggggca ggggtgccaa ttttagcatt tctgaagac 900
atcttctat cagcagtcac aacacaagtc gcagaaacta accaccgaca ccaggcaaga 960
acaagacggc caagagctct ccggggcgct gcctttatag ccagtaggga tctcgccaca 1020
gtcggaaacg acgggggtgc cggagtagga

```

1050

002221 004E2960



## (2) INFORMATION ON SEQ ID NO. 29:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 581 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

caggcttcct tctggcaaca ggcgtgggtc acgctctcgc tcggtctttc tgccgccatc 60
ttggttcgcg gttccctgca caaaatgccc ggcgaacacc agaaaccgtc cctgctacag120
agcaggagtt gccgcagccc caggctgaga cagggtctgg aacagaatct gacagtgatg180
aatcagtacc agagcttgaa gaacaggatt ccaccaggc aaccacacaa caagcccagc240
cggcggcagc agctgaaatc gatgaagaac cagtcagtaa agcaaaacag agtcggagtg300
aaaagaaggc acggaaggct atgtccaaac tgggtcttcg gcaggttaca ggagttacta360

gagtcactat ccggaaatct aagaatatcc tctttgtcat cacaaaaacca gttgtctaca420
agagccctgc ttcagatacg tacatagttt ttggggaagc cagatcgaag attatcccag480
caagcacaaac tagcagctgc tgagaagtca agttcagggt aactgtctca acgttcagga540
aaccctccggc ttccactgta gagggggagc aaggggaggg t
581

```

## (2) INFORMATION ON SEQ ID NO. 30:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 264 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

09673400.122700

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

gggactatgt tgtgagcctg cgaaagaagt ttgtgtgggg actgtgggca gtgaatgcgt 60
tgggaacaat atggaaaact gggagctgcc ctcagtttct cccaagtgt gactcacttt120
cggggtgtcc caaaagcctg attccagggc ctgctagccc gaccccggtg acgcctccac180
ccgcgcctgg cccagcctt caccgcgat cgccgccctc cggggcacac ctcgcgcag240
aaaacagccg gcgggcggcg agac                                     264

```

## (2) INFORMATION ON SEQ ID NO. 31:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 111 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

cggcgaatca cttataaatg gcgcgaagc aggagcccga aggctaaatt gcaggagggg 60
tgagcgaatg ctgtgctttc atgggcctct tacgttgatg aggcaaagta t      111

```

## (2) INFORMATION ON SEQ ID NO. 32:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 76 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

00673400.12900

(vi) ORIGIN  
(A) ORGANISM: HUMAN

PFCEETKTER LWPRCRPPAA VGFSTQNPV GDSSENLFLSL PFLGSKANPI PTHWSSALIF60  
NLPSPPFQNT HIPFQN 76

SSFLFSFQTQ FHKNRKDKVF SSRQAKPFPH HQSILKIHEE VERSVSGRLK GSSSSNPTAA60  
EKIEIEILKI TS 72

KKLDYFCAEI KNSHCKTKIK IAQIRKPGGG KCQVSKVHEF SLSKRSSTKT ARIKFSVADK60  
QSPFHIINQS 70

## (2) INFORMATION ON SEQ ID NO. 35:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

SSGPAPGCSP FAGTRKNFPS MVVLERTFLK INYIFLCIPM EFQFIRCSPW PPQNTVIPA60

## (2) INFORMATION ON SEQ ID NO. 36:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ASGVHTETHR YNLLSAKSRK KGWGYLGWLG FDFLLVCLFC TKTVLSFEYR RDISIYMLSN60  
QDG 63

## (2) INFORMATION ON SEQ ID NO. 37:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 170 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

002221-004E2950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

(2) INFORMATION ON SEQ ID NO. 38:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
ARAPTLDMRF RRRLSADPHA TQRNSAEARG TMDGRVQLMK ALLAGPLRPA ARWRNPIPF 60
PETFDGDTDR LPEFIVQTCS YMFVDENTFS NDALKVTFLI TRLTGPALQW VIPYIRKESPI20
LINDYRGELA EMKRVEGWEE DEDF                                     144
```

(2) INFORMATION ON SEQ ID NO. 39:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 178 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

HSLGRAPVET LAVATGTANS SQSTRPQARG SPGLEVLVLL PSKDSLHLGQ KAPVIEQGA 60  
LLPDVGDHPL QGWPKEAGDE ERHLQGVVGE RVLVHEHVGA RLHDELRESV GISVKRLGKG120  
NRVFPATRRG PEGPGQEGH QLHPTVHRAA RLRGVSLGCV GVSASAKSPE HVEGGGPG 178

## (2) INFORMATION ON SEQ ID NO. 40:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 89 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

KLTGINTGCR NMLALCIRGH AQIQEIYLA TFSRKGTLGI IHVILEVFLG FFFFFLRQSC60  
CIAQAGSVVA QSQLIASSIT QGLSNPPTL 89

## (2) INFORMATION ON SEQ ID NO. 41:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 95 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

IVTWRKVPMS LCQRPPPFVR IGIFRLKGL AHIRCDLFIP VVMEGHICQS LESAKAGTRF60  
PGPQWGCANP RELGCKFVKV QHHVWQLSIG ARSLP 95

## (2) INFORMATION ON SEQ ID NO. 42:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 154 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

002221 0042960

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CQLVFRIQTD GSYWSLGLTS SGNITFSWAE MLLPALKQHS VLKTSWQAPG SNTQLPNMML 60  
ILHEFATQFS RVCTPPLWAG EPGPGLRRLQ ALADVALHNN GNEKVTPYVR QALKESEYPN120  
PHKRRGTLAK THGNFPPSND LDRRATQDSP SCSV 154

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 79 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

LASTLGVETC LPYVSEDMLS RSKRYIWQLF LEKAHWVSFI TFLSFFGFFF FFFETVLLYC60  
PGWSVVAQSQ LIASSITQA 79

(2) INFORMATION ON SEQ ID NO. 44:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 82 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CQLVFRIQTD GSYWSLGLTS SGNITFSWAE MLLPALKQHS VLKTSWQAPG SNTQLPNMML60  
ILHEFATSWL PRLQHSVGT QS 82

002221 004E/960

## (2) INFORMATION ON SEQ ID NO. 45:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 68 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

RGSKDRNSGQ GSGSYGQLSC RGFSDQFSRV CTFPLWAGEP GPGLRRLQAL ADVALHNNNGN60  
EKVTPYVR 68

## (2) INFORMATION ON SEQ ID NO. 46:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 87 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

DYVVS LRKKF VWGLWAVNAL GTIWKTGSCP QFLPKLOSLS GCPKSLIPGP ASPTPVTPPP60  
APGPSLHPRS PPSGAHPPE NSRRAAR 87

## (2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 51 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

007221-004E2950



(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

QALSGFWDY PKVSPTWGET EGSSQFSILF PTHSLPTVPT QTSFAGSQHS P

51

(2) INFORMATION ON SEQ ID NO. 48:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 20 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

RRITYKWRRS RSPKAKLQEG

20

(2) INFORMATION ON SEQ ID NO. 49:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 36 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GESLINGAEA GARRLNCRRG ERMCLFHGPL TLMRQS

36

00/22/97 00:42:00

## (2) INFORMATION ON SEQ ID NO. 50:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

KHSIRSPLLQ FSLRAPASAP FISDSP

26

## (2) INFORMATION ON SEQ ID NO. 51:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

EAHESTAFAH PSCNLAFGLL LRRHL

25

## (2) INFORMATION ON SEQ ID NO. 52:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3665 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

006673400.122700

(iii) ANTI-SENSE: NO

(A) ORGANISM: HUMAN

(C) ORGAN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GGCCATTTTGG	TGAAGAGACG	AAGACTGAGC	GTTGTGGCC	GCGTTGCCGA	CCTCCAGCAG	60
CAGTCGGCTT	CTCTACGCAG	AACCCGGGAG	TAGGAGACTC	AGAAATCGAA	TCTCTTCTCC	120
CTCCCCTTCT	TGGGCAGCAA	GGCGAACCCC	ATCCCTACTC	ACTGGAGCTC	AGCTTTGATT	180
TTTAACCTCC	CTTCCCCACC	CTTCCAGAAT	ACACACATTC	CATTCCAAAA	CTGATTTTAT	240
AAAGACATTT	TAAACATAAT	GATGCAACTT	GGTGTGCACT	ACAGCAAATG	TACAGGTGTT	300
TTTTTTTTAA	TGTGTTCCAA	AACCGGGACC	TGGATTTAAG	ATGTAATTTT	TAAATTTTCT	360
ATTTCTATTT	TTTCTGCAGC	AGTTGGGTTA	GAGGAGGAGG	AGCCTTTTAG	CCTCTCATAA	420
ACTGACCTCT	CTACTTCCTC	GTGTATTTTT	AAGATTGATT	GATGATGTGG	AAAGGGCTTT	480
GCTTGTCTGC	TACTGAAAAC	TTTATCCTGC	GGTTTTGTG	GAAACTGCTT	TTGGAAAGAG	540
AAAAGAAATG	AACTTTACTG	ACTTGACATT	TTTGCACCTC	CCGTTTTTCT	AATCTGGGCT	600
ATTTTTATTT	TTGTTTTTTT	ACAGTGAGAT	TTTTTTGATC	TTCAGCTTAC	ATTTTCGGGC	660
TTTGTGAGGA	AACCTTTTACC	CATCAAACAC	GATGGCCAGC	AACGTTACCA	ACAAGACAGA	720
TCCTCGCTCC	ATGAACCTCC	GTTATTTCAT	TGGGAATCTC	AACACTCTTG	TGGTCAAGAA	780
ATCTGATGTG	GAGGCAATCT	TTTCGAAGTA	TGGCAAAATT	ATGGGCTGCT	CTGTTTCATAA	840
GGGCTTTGCC	TTCGTTCACT	ATGTTAATGA	GAGAAATGCC	CGGGCTGCTG	TAGCAGGAGA	900
GGATGGCAGA	ATGATTGCTG	GCCAGGTTTT	AGATATTAAC	CTGGCTGCAG	AGCCAAAAGT	960
GAACCGAGGA	AAAGCAGGTG	TGAAACGATC	TGCAGCGGAG	ATGTACGGCT	CCTCTTTTGA	1020
CTTGGAATAT	GACTTTCAAC	GGGACTATTA	TGATAGGATG	TACAGTTACC	CAGCACGTGT	1080
ACCTCCTCCT	CCTCCTATTG	CTCGGGCTGT	AGTGCCCTCG	AAACGTGAGC	GTGTATCAGG	1140
AAACACTTCA	CGAAGTGGCA	AAAGTGGCTT	CAATTCTAAG	AGTGGACAGC	GGGGATCTTC	1200
CAAGTCTGGA	AAAGTTGAAAG	GAGATGACCT	TGAGGCCATT	AAGTAAGAGC	TGACCCAGAT	1260
AAAAACAAAA	GTGGATTCTC	TCCTGGAAAA	CCTGGAAAAA	ATTGAAAAGG	AACAGAGCAA	1320
ACAAGCAGTA	GAGATGAAGA	ATGATAAGTC	AGAAGAGGAG	CAGAGCAGCA	GCTCCGTGAA	1380
GAAAGATGAG	ACTAATGTGA	AGATGGAGTC	TGAGGGGGGT	GCAGATGACT	CTGCTGAGGA	1440
GGGGGACCTA	CTGGATGATG	ATGATAATGA	AGATCGGGGG	GATGACCAGC	TGGAGTTGAT	1500
CAAGGATGAT	GAAAAAGAGG	CTGAGGAAGG	AGAGGATGAC	AGAGACAAGG	CCAATTGGCGA	1560
GGATGACTCT	TAAGCACATA	TGTTGGGTTA	GAAATCTTAT	CCCATTATTT	CTTTACCTAGT	1620
CGCGTTGTCT	TAAGTCAAAAT	TTTTCACCAG	ATCCTCTCCC	CTAGTATCTT	CAGCACAATG	1680
TCACTGTTCT	CCCCATCCTT	GTCTTCCCA	TGTTTCATTAA	TTCATATTGC	CCCGCGCCTA	1740

GTCCCATTTT CACTTCCTTT GACGCTCCTA GTAGTTTTGT TAAGTCTTAC CCTGTAATTT1800  
 TTGCTTTTAA TTTTGATACC TCTTTATGAC TTAACAATAA AAAGGATGTA TGGTTTTTAT1860  
 CAACTGTCTC CAAAATAATC TCTTGTTATG CAGGGAGTAC AGTTCTTTTC ATTCATACAT1920  
 AAGTTCAGTA GTTGCTTCCC TAACTGCAAA GGCAATCTCA TTTAGTTGAG TAGCTCTTGA1980  
 AAGCAGCTTT GAGTTAGAAG TATGTGTGTT ACACCCTCAC ATTAGTGTGC TGTGTGGGGC2040  
 AGTTCAACAC AAATGTAACA ATGTATTTT GTGAATGAGA GTTGGCATGT CAAATGCATC2100  
 CTCTAGAAAA ATAATTAGTG TTATAGTCTT AAGATTTGTT TTCTAAAGTT GATACTGTGG2160  
 GTTATTTTTG TGAACAGCCT GATGTTTGGG ACCTTTTTTC CTCAAATAA ACAAGTCCTT2220  
 ATTAAACCAG GAATTTGGAG AAAAAAAAAA AAAAAAATTT TTTATTTTTG TATTTTATTA2280  
 TTGTTTACTT CAAACTTTGT TTTACAGCGT CCTCCACAAA ACCTCTAGAA TGCATAGAT2340  
 ATATTTTTCT TGGAGTCATA ATCATGATGC ATACCAACAC AACACTACTC AAATTATATT2400  
 TCATTGAGAT GCATGTTGCA TTGAGGAGTC AACTTGACAT AGAGTGGAGA CTTTTTCAA2460  
 ATGGCTTTTA CATCCTAATG AAAGTTTGGG AAGTATATCC TCTCTGCCTT TTCATCAGTG2520  
 CTTTGTGGTC CAGCTGGCAC CCTTCTGAG GTTTGTGTTT TGTGCTAAAT GGTTTTGTCC2580  
 TTAAATAGGA GAGGCTCAAA AACATCAAGA TTTCAGGAAA ATGGCGACAC TGGCATAATG2640  
 GAACCCCTT GCTTCTATTT TGTTCTTTTA ATTACTATTT ATAGCCCCAG TTACCTTCTG2700  
 AATTCTGAAG TGTATATACC TCCATGTTCC TGAAAACAAG AAAACTCTTA CTTCTGATA2760  
 TTCCATAGAC TGCCTTCCCA GGTGATTGAG AACATAGAGA ATGTTACACA TTTATTTTAC2820  
 TCTAAATGAT CTTTTACCCC TGTTAGCTAA TCTTTGTGTT TTCCTCAACT TTATTAATTA2880  
 CAGTGATTGC ATTTTTAGCA TCCAGTTGTA AGATGAATAT ATTAAACAGC TACCAGTGTT2940  
 GGTGATACCT CATCCTTGAA AGGCTTAGTT CATTTGTGTT TTATACTTCA GTTTTTCCAG3000  
 CATAGCAGAA AATGCCGCTT ATAATTTTGT TGCACACAAA CCTTGGAAATC CCCCTGTAAA3060  
 GTTGCTATGG TTTCATAGCA TGCGGCACTG GCCCCTTTTT CATCCCACTC ATTACAGGCA3120  
 AAACCCATGT CTTATTTATG AGGATTTTAT AGATCATTTT CTGTAACAGG TGACAAAAGC3180  
 AGAAAAGAAT GAAGAGGCTG AAGTATGAAC TACCCTTGGA GCCCATATAC ATGATATAGG3240  
 CAATTTCTTT TGTATGTTAA TTCAGTCAAA AATACTACCC ACTTGATGTT TTCTAATCTG3300  
 ATGTGAGCTC ATGTTACACA GACTTTTAGT AAGTAACCCG TGACTAGAAA ATAAACTGGA3360  
 TGCTTAGGAG AGAGTGTGAG ATGTATAAGA TGCTAATAAA ACCTGTTTAA TATTATTGTT3420  
 AGCTGTAAGT TTTTGGGAAA TACTGAACAA ATTAGTCCAC AATCAAGTGT CTACTTTTCC3480  
 CTTCACTGTA GGGCCTCTCC CTGCACAGAG CAGTCTGTTT AGCTGTGAAC ACCACAATCT3540  
 GCAGATGTTT AAGTCCCTTA CATAAAATGG CATAGTATTT ATATGTAACC TATGCATATT3600  
 CTCCTGTATA TTTTAAATCA TCTCTACATT AAAATACCTG ATAAATCTA AATAAAAAAA3660  
 AAAAA 3665

## (2) INFORMATION ON SEQ ID NO. 53:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 301 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GNLYPSNTMA SNVTNKTDPK SMNSRVFIGN LNTLVVKKSD VEAIFSKYK IVGCSVHKGF 60  
 AFVQYVNERN ARAAVAGEDG RMIAGQVLDI NLAAEPKVNK GKAGVKRSAA EMYGSSFDDL120  
 YDFQRDYDR MYSYPARVPP PPPIARAVVP SKRQRVSGNT SRGKSGFNS KSGQRGSSKS180  
 GKLGDDLQA IKKELTQIKQ KVDSLLENLE KIEKEQSKQA VEMKNDKSEE EQSSSVKKD240  
 ETNVKMESEG GADDSAEEDG LLDDDDNEDR GDDQLELIKD DEKEAEEGED DRKANGEDD300  
 S 301

## (2) INFORMATION ON SEQ ID NO. 54:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

ESSSPALALSL SSSPSSASFS SSLINSSWSS PRSSLSSSSS RSPSSAESSA PPSDSIFTLV 60  
 SSFFTLLLC SSSDLSFFIS TACLLCSFSI FSRFSRREST FCFIWSSFL MA 112

## (2) INFORMATION ON SEQ ID NO. 55:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TRNLEKKKKK NLFLEYFIIV YFKLCFTASS TKPLECTRYI FLGVIIMMHT NTTLLKLYFI 60  
 EMHVALRSQ L DIEWRLFQNG FYILMKVWEV YPLCLFISAL WSSWHPF 107

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WO 99/54448

PCT/DE99/01178

**Claims**

1. A nucleic acid sequence that codes a gene product or a portion thereof, comprising

- a) a nucleic acid sequence, selected from the group Seq. ID Nos. 14-18, 30, 31, and 52,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 14-18, 30, 31, 52, or a complementary or allelic variant thereof.

3. Nucleic acid sequence Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52, characterized in that it is expressed elevated in hystero myomic tissue.

4. BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52 for use as vehicles for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has 95% homology to a human nucleic acid sequence.

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7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a sufficient amount that they hybridize with the sequences according to claims 1 to 6.

8. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

15. A DNA fragment, comprising a gene, that can be obtained from the use according to claim 14.

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16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to one of claims 16 or 17, wherein the prokaryotic cell system is E. coli, and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 16 to 18 are cultivated.

20. An antibody that is directed against a polypeptide or a fragment that is coded by the nucleic acids of sequences Seq. ID Nos. 1-31 and Seq. ID 52, which can be obtained according to claim 19.

21. An antibody according to claim 20, wherein it is monoclonal.

22. An antibody according to claim 20, wherein it is a phage display antibody.

23. Polypeptide partial sequences according to sequences Seq. ID Nos. Seq. 32-51 and Seq. ID Nos. 53-55.

24. Polypeptide partial sequences according to claim 23, with at least 80% homology to these sequences.

25. A polypeptide that is known from a phage display and that can bind to the polypeptide partial sequences according to claim 23.

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26. Polypeptide partial sequences according to claim 23, with at least 90% homology to these sequences.

27. Use of polypeptide partial sequences according to sequences Seq. ID Nos. 32 to 51 and Seq. ID Nos. 53-55 as tools for finding active ingredients against hystero myoma.

28. Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-31 and Seq. ID No. 52 for expression of polypeptides that can be used as tools for finding active ingredients against hystero myoma.

29. Use of nucleic acid sequences Seq. ID Nos. 1-31 and Seq. ID No. 52 in sense or antisense form.

30. Use of polypeptide partial sequences Seq. ID No. 32 to Seq. ID No. 51 and Seq. ID Nos. 53-55 as pharmaceutical agents in gene therapy for treatment of hystero myoma.

31. Use of polypeptide partial sequences Seq. ID No. 32 to Seq. ID No. 51 and Seq. ID Nos. 53-55 for the production of a pharmaceutical agent for treatment of hystero myoma.

32. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID No. 32 to Seq. ID No. 51 and Seq. ID Nos. 53-55.

33. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.

34. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.

35. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that

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can be obtained from cDNAs of sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52.

36. Use of the genomic genes according to claim 33, together with suitable regulatory elements.

37. Use according to claim 36, wherein the regulatory element is a suitable promoter and/or enhancer.

38. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 300 to 3500 bp.

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## Systematic Gene Search in the Incyte LifeSeq Database

Normal tissue  
~50,000 individual ESTs

Tumor tissue  
~50,000 individual ESTs

Priority list  
High

Prostate  
Breast  
Ovary  
Bladder  
Uterus

Iterative assembling  
with  
increasing mismatch

Low

~8,000 contigs  
+  
~25,000 individual  
sequences

~8,000 contigs  
+  
~25,000 individual  
sequences

## Comparison of databases

normal tissue-  
specific  
(expected: 100-500)

nonspecifically  
expressed genes

tumor tissue-  
specific  
(expected: 100-500)

Genes of Interest

Figure 1

REPLACEMENT PAGE (RULE 26)

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## Systematic Gene Search in the Incyte LifeSeq Database

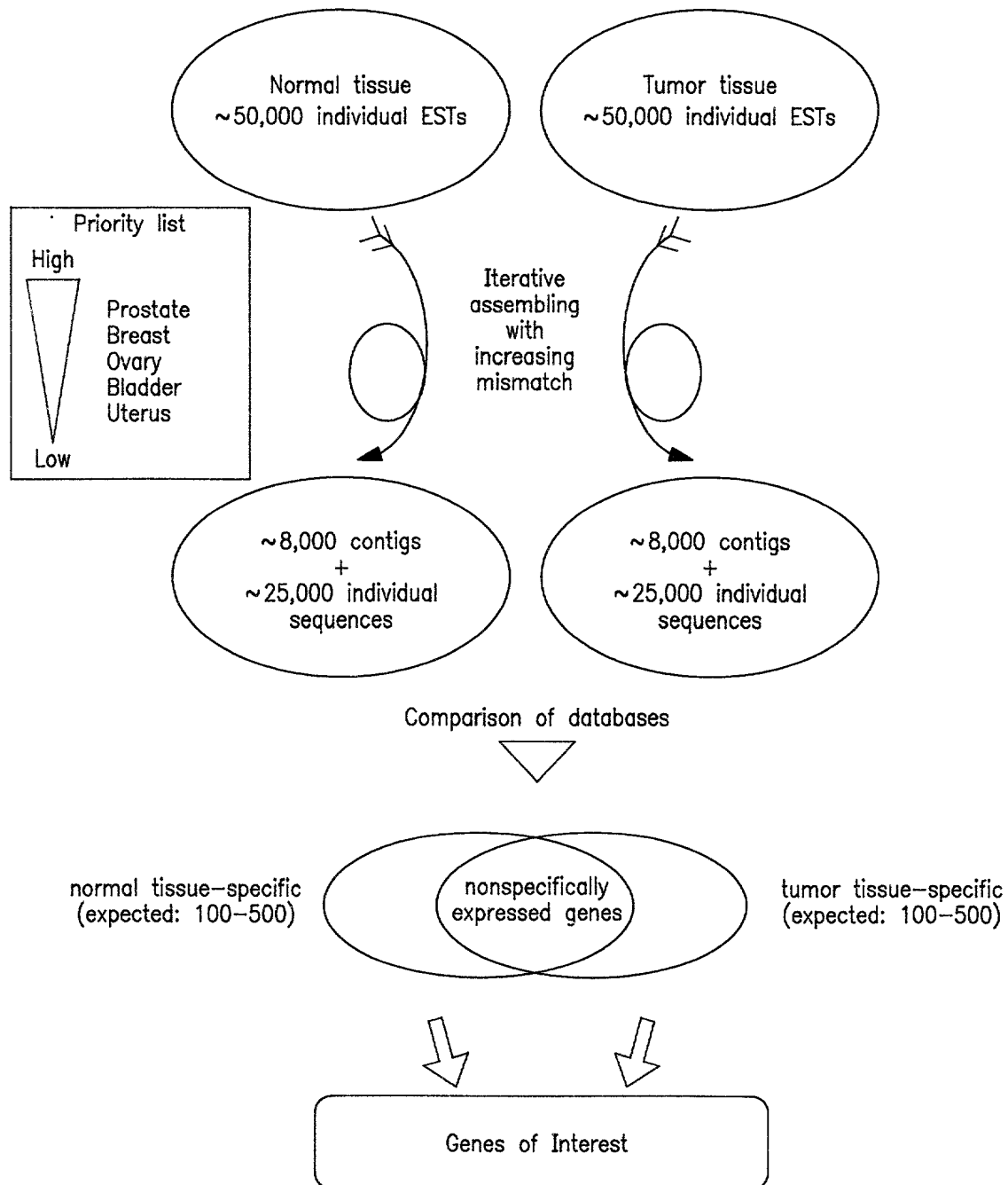


FIG. 1

## Principle of EST Assembly

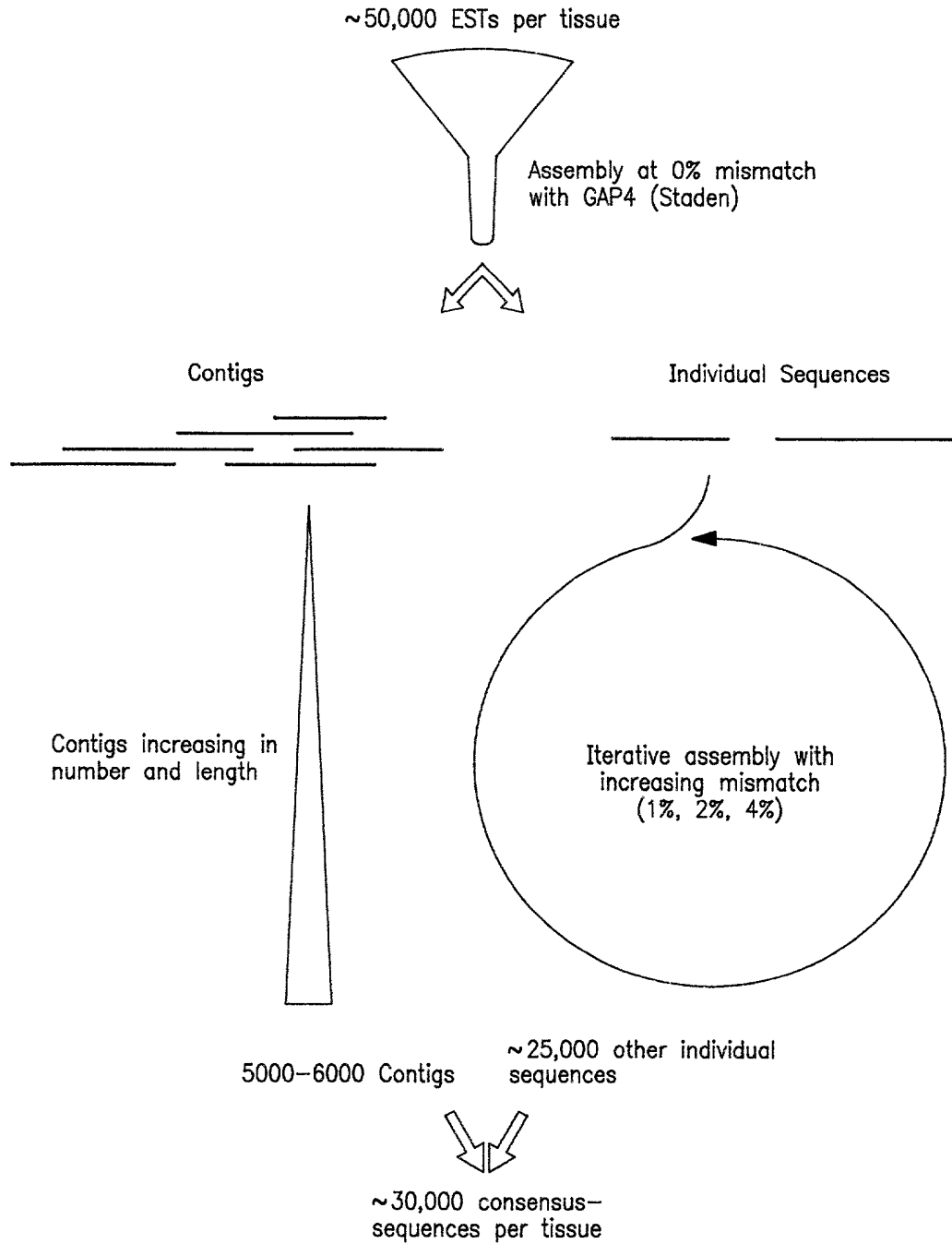


FIG. 2a

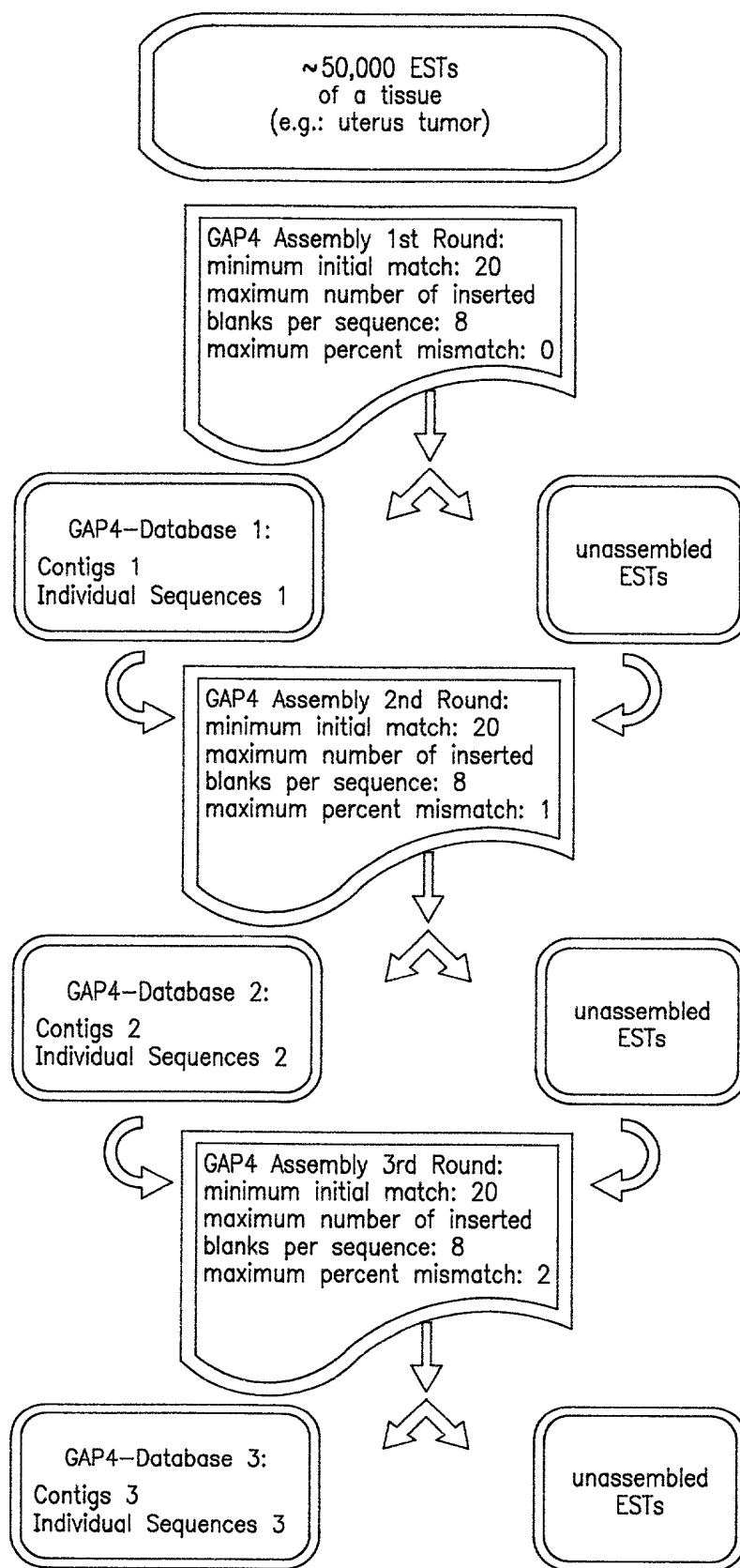


FIG. 2b-I

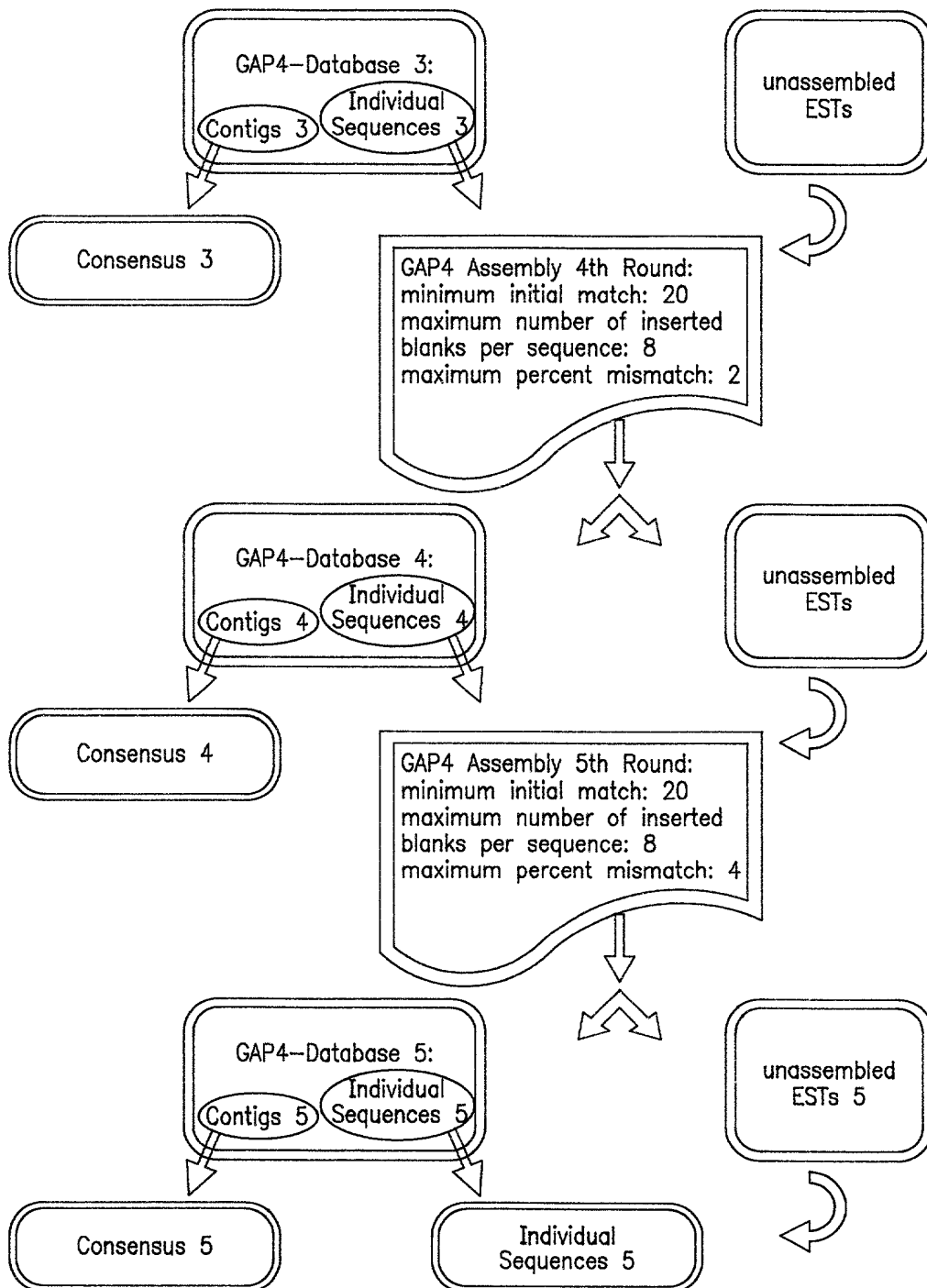


FIG. 2b-2

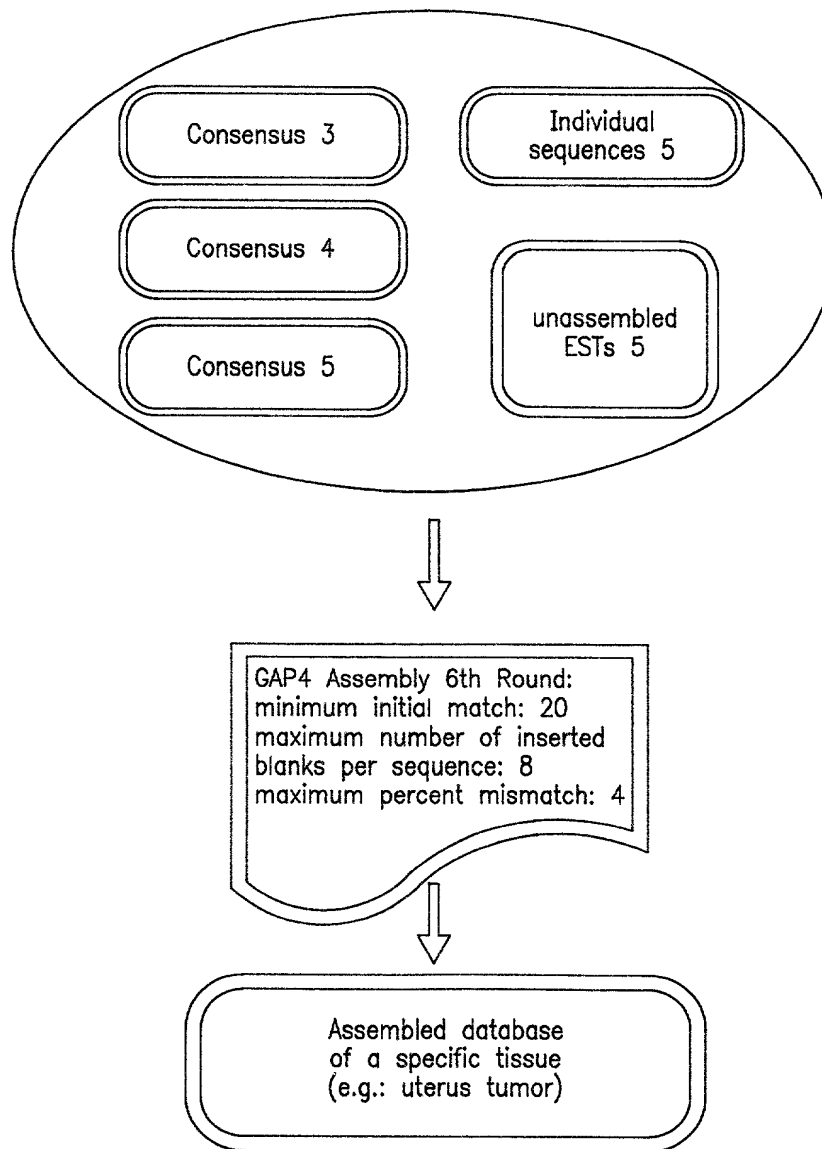


FIG. 2b-3



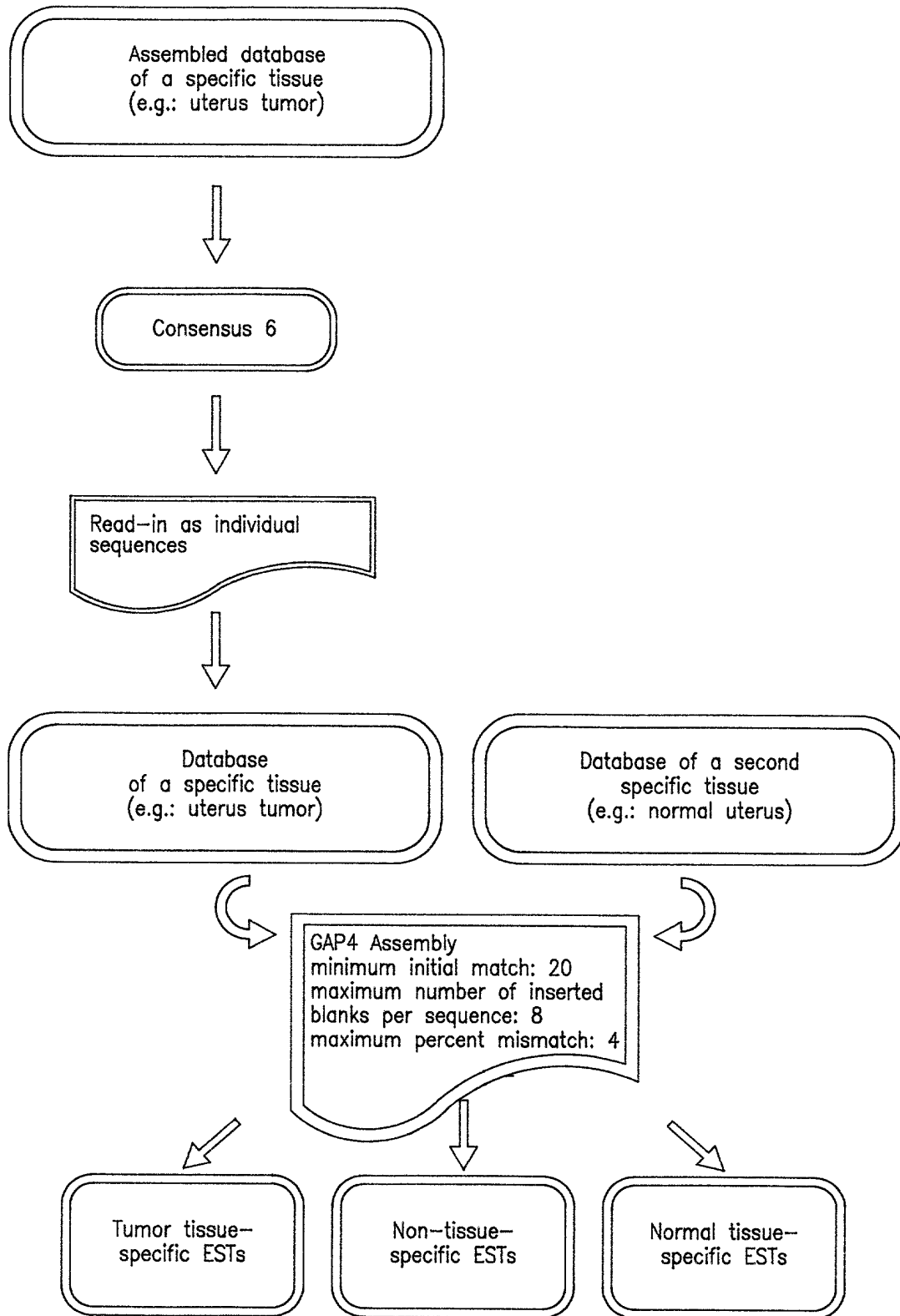


FIG. 2b-4

In silico subtraction of gene expression in various tissues

~30,000 consensus sequences  
normal tissue

~30,000 consensus sequences  
tumor tissue

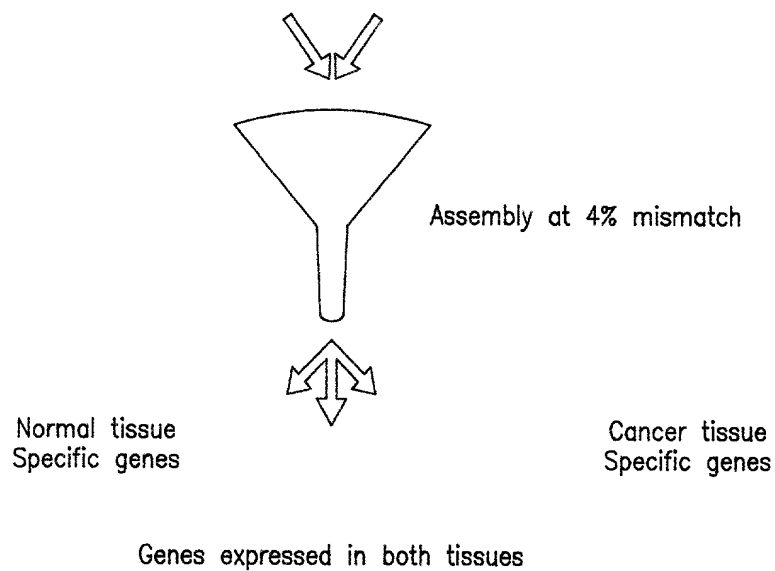


FIG. 3

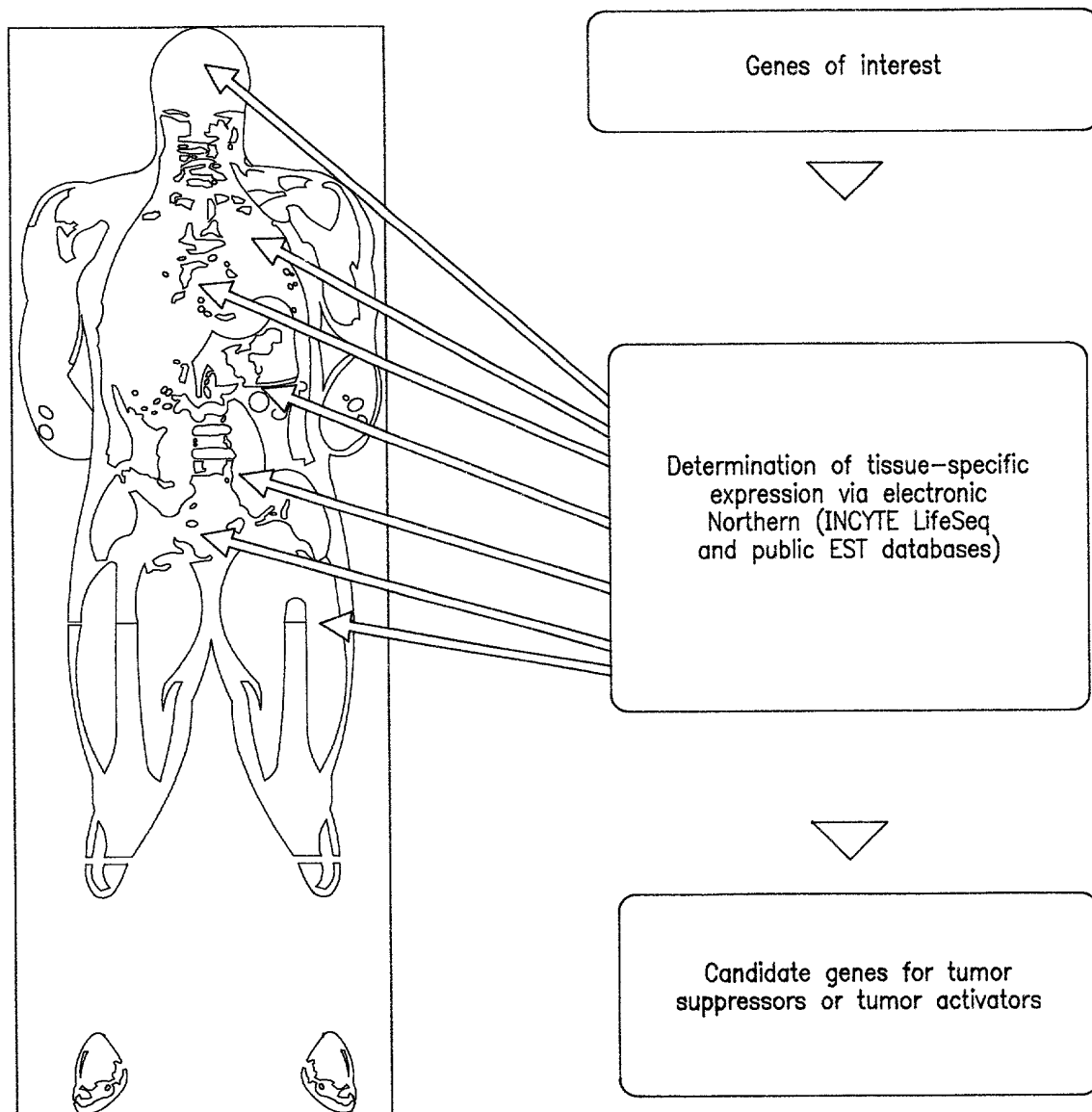


FIG. 4a

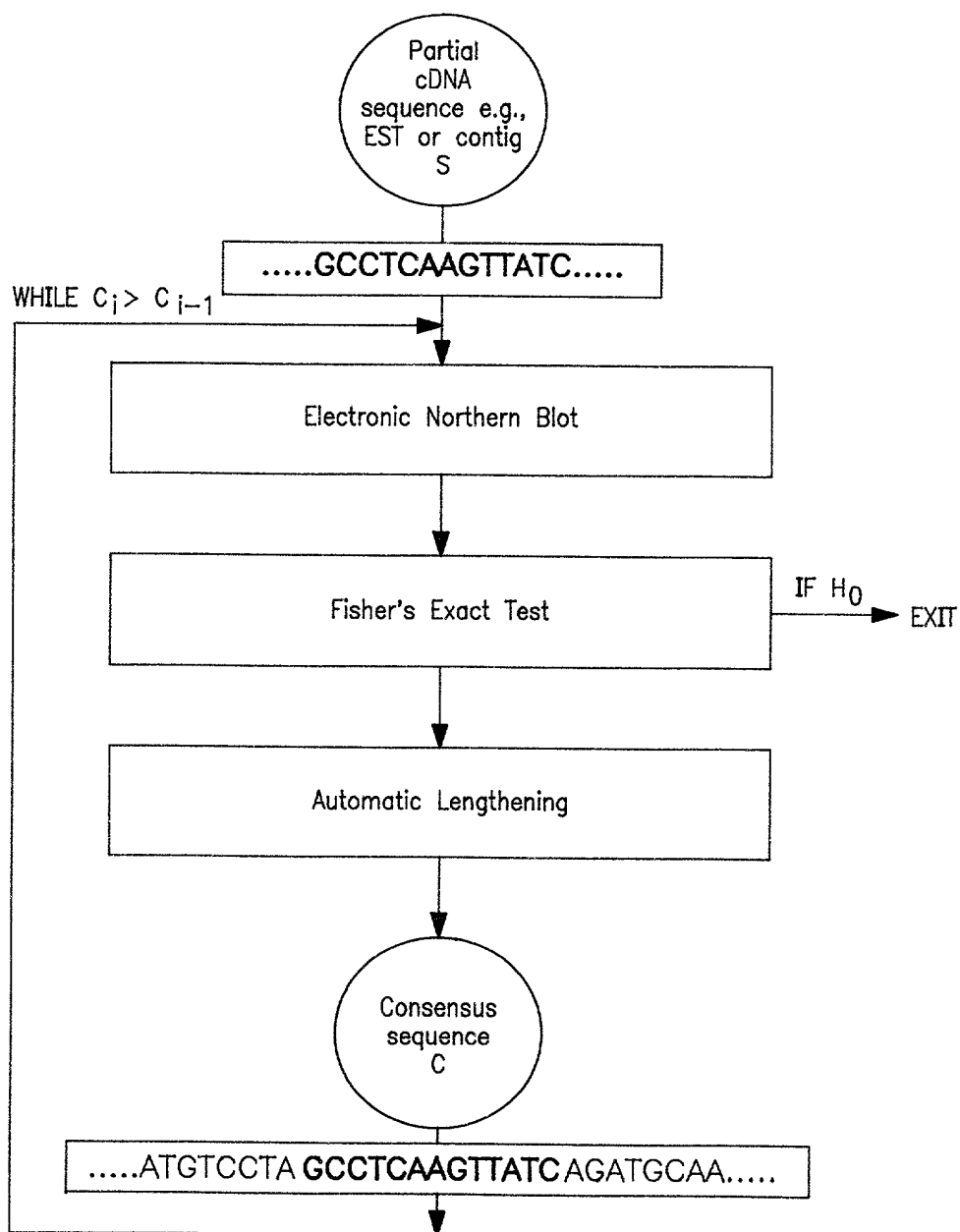


FIG. 4b

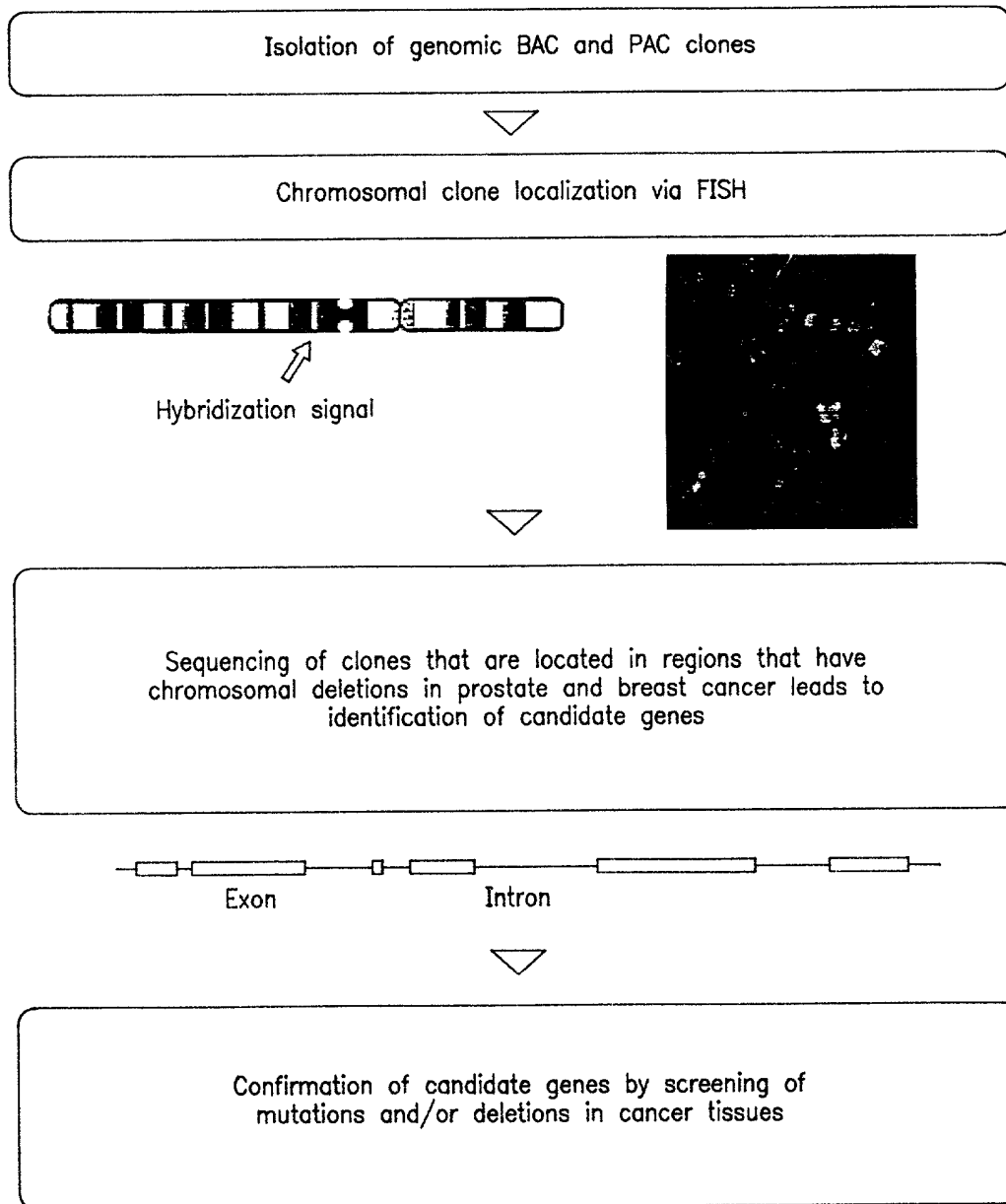


FIG. 5

## DECLARATION FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

## HUMAN NUCLEIC ACID SEQUENCES OF UTERUS MYOMA TISSUE

the specification of which

☐ is attached hereto

☒ was filed on 15 April 1999 as United States Application Number or PCT International Application Number PCT/DE99/01178 and (if applicable) was amended on \_\_\_\_\_

I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56.

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed.

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119			
APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 17 947.2	Germany	17 April 1998	X

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)	
APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120		
APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

14 I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Alan E.J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brion P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Nancy J. Axelrod (44,014); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that wilful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such wilful false statements may jeopardize the validity of the application or any patent issued thereon.

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